

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2005, 15:51:19 ; Search time 38.4375 Seconds
(without alignments)
50.310 Million cell updates/sec

Title: US-10-614-959-10

Perfect score: 29

Sequence: 1 TYAMH 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	29	100.0	5	3	AAY79068	Aay79068 Anti-fact
2	29	100.0	7	3	AAB14789	Aab14789 Aspergill
3	29	100.0	12	3	AB14784	Ab14784 Aspergill
4	29	100.0	120	4	AA65570	AA65570 Amino aci
5	29	100.0	121	5	ABG76537	ABg76537 HCV E1 an
6	29	100.0	128	5	ABG76559	ABg76559 HCV E1 an
7	29	100.0	206	6	ABU24807	ABu24807 Protein e
8	29	100.0	258	7	ABO77482	ABo77482 Pseudomon
9	29	100.0	278	8	ADN27332	ADn27332 Bacterial
10	29	100.0	307	4	AA672483	AAg72483 Human OR-
11	29	100.0	321	4	AA671475	AAg71475 Human olf
12	29	100.0	531	8	ADR10293	ADr10293 Human pro
13	29	100.0	690	3	AA550844	AAy50844 A. oryzae
14	29	100.0	690	3	AA550835	AAy50835 A. oryzae
15	29	100.0	703	3	AB14781	AB14781 Aspergill
16	29	100.0	703	3	AB14782	AB14782 Aspergill
17	26	89.7	46	4	AAW82576	AAm82576 Human imm
18	26	89.7	67	4	AB40299	ABb40299 Peptide #
19	26	89.7	67	4	AA33985	AAm33985 Peptide #
20	26	89.7	67	4	AAW73798	AAm73798 Human bon
21	26	89.7	67	4	AAW61093	AAm61093 Human bra
22	26	89.7	67	4	ABG55546	ABg55546 Human liv
23	26	89.7	67	5	ABG43685	ABg43685 Human pep
24	26	89.7	79	4	AAU18208	AAu18208 Novel hum
25	26	89.7	79	5	ABG92629	ABg92629 Human DNA

26	26	89.7	79	7	ADC25346	Adc25346 Human ext
27	26	89.7	89	5	ABG68752	ABg68752 Cytochrom
28	26	89.7	162	5	ABP01422	ABp01422 Human ORF
29	26	89.7	173	5	ABG68756	ABg68756 Cytochrom
30	26	89.7	194	7	AD808218	Ad808218 Novel pro
31	26	89.7	205	7	AD808219	Ad808219 Novel pro
32	26	89.7	213	5	ABB91152	Abb91152 Herbicida
33	26	89.7	221	6	ADA55412	Ada55412 Human pro
34	26	89.7	238	5	ABP46042	ABp46042 Human Bly
35	26	89.7	238	7	ADG96869	Adg96869 Single ch
36	26	89.7	242	5	ABB49910	Abb49910 Listeria
37	26	89.7	304	6	ABU17641	ABu17641 Protein e
38	26	89.7	370	4	AA691423	AAg91423 C glutami
39	26	89.7	370	4	AA690014	AAg90014 C glutami
40	26	89.7	454	7	ABO63767	ABo63767 Klebsiell
41	26	89.7	455	7	ADF08003	Adf08003 Bacterial
42	26	89.7	501	8	ADO47242	Ado47242 Rabbit cy
43	26	89.7	502	5	AAE26192	AAe26192 Human cyt
44	26	89.7	502	7	ADE57186	Ad57186 Human Pro
45	26	89.7	502	7	ADE57190	Ad57190 Human Pro

ALIGNMENTS

RESULT 1

AAAY79068

ID AAY79068 standard; peptide; 5 AA.

XX AC AAY79068;

XX AC AAY79068;

DT 12-JUN-2000 (first entry)

XX DE

XX DE

XX DE

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Anti-factor IX/IXa antibody H chain V domain CDR1 amino acid sequence.
Complementarity determining region 1; CDR1; antibody; Gla domain;
factor IX/IXa; blood coagulation; deep venous thrombosis;
arterial thrombosis; unstable angina; post myocardial infarction;
coronary artery bypass graft; CABG; stroke; tumour growth; metastasis;
percutaneous transluminal coronary angioplasty; PTCA; inflammation;
septic shock; hypotension; adult respiratory distress syndrome; ARDS;
arterial fibrillation; disseminated intravascular coagulopathy; DIC.

Homo sapiens.

WO200012562-A1.

09-MAR-2000.

26-AUG-1999; 99WO-US019453.

28-AUG-1998; 98US-0098233P.

03-MAR-1999; 99US-0122767P.

(GETH) GENENTECH INC.

Adams CW, Devaux B, Eaton DL, Hass PE, Judice JK, Kirchhofer D;

Suggatt S;

WPI; 2000-256595/22.

Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-

carboxyglutamic acid domains useful as anti-coagulant in thrombosis,

stroke, and post myocardial infarction.

Claim 2; Fig 2; 84pp; English.

This sequence represents a complementarity determining region 1 (CDR1) of

the heavy chain variable domain of a human anti-factor IX/IXa Gla domain

antibody. Factor IXa is a vitamin K dependent plasma serine protease that

participates in the blood coagulation pathways. The Gla domain of factor

IXa and its zymogen factor IX contains important structural determinants

for interaction with high affinity binding sites on vascular endothelial

CC cells and platelets. Compositions comprising the antibodies are used for
 CC the treatment or prophylaxis of thrombotic or coagulopathic diseases or
 CC disorders in a mammal for which inhibiting a FIX/IXa mediated event is
 CC indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable
 CC angina, post myocardial infarction, post surgical thrombosis, coronary
 CC artery bypass graft (CABG), percutaneous transluminal coronary
 CC angioplasty (PTCA), stroke, tumour growth, invasion or metastasis,
 CC inflammation, septic shock, hypotension, adult respiratory distress
 CC syndrome (ARDS), arterial fibrillation and disseminated intravascular
 CC coagulopathy (DIC)
 XX
 SQ Sequence 5 AA;

Query Match 100.0%; Score 29; DB 3; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
 |||||
 Db 1 TYAMH 5

RESULT 2
 AAB14789
 ID AAB14789 standard; peptide; 7 AA.
 XX
 AC AAB14789;
 XX
 DT 06-DEC-2000 (first entry)
 XX
 DE Aspergillus oryzae KBN616 glutaminase peptide, SEQ ID NO:12.

XX Glutaminase; Aspergillus oryzae KBN616; glutamic acid synthesis;
 KW fermentation; foodstuff production; miso; soy sauce; peptide fragment;
 KW PCR primer design.
 XX
 OS Aspergillus oryzae.

XX JP2000166547-A.
 XX 20-JUN-2000.
 XX 07-DEC-1998; 98JP-00347127.
 XX 07-DEC-1998; 98JP-00347127.
 XX (AICH-) AICHI KEN PREFECTURE.
 PA (ICHI-) ICHIBIKI KK.
 XX
 DR WPI; 2000-477931/42.
 XX
 PT A new glutaminase and its preparation.
 XX
 PS Example 2; Page 25; 27pp; Japanese.

CC The invention relates to two novel glutaminases (AAB14781, AAB14782) from
 CC Aspergillus oryzae KBN616 and Aspergillus sojae BA-104 respectively which
 CC have molecular weights of approximately 73 kD (as determined by gel
 CC filtration). The enzymes have an optimum temperature of approximately 50
 CC degrees Celsius, and an optimum pH of about 8.5. The glutaminases
 CC catalyse the conversion of L-glutamine to L-glutamic acid, and may be
 CC used in the production of fermented foodstuffs such as soy sauce and
 CC miso. Sequences AAB14781-B14789 represent fragments of Aspergillus oryzae
 CC KBN616 glutaminase which were used as the basis for the design of
 CC degenerate PCR primers AAA72206, AAA72207 and AAA72209. These primers
 CC were used in the isolation of genomic DNA encoding Aspergillus oryzae
 CC KBN616 (AAA72204)
 XX
 SQ Sequence 7 AA;

Query Match 100.0%; Score 29; DB 3; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
 |||||
 Db 3 TYAMH 7

RESULT 3
 AAB14784
 ID AAB14784 standard; peptide; 12 AA.
 XX
 AC AAB14784;
 XX
 DT 06-DEC-2000 (first entry)
 XX
 DE Aspergillus oryzae KBN616 glutaminase peptide fragment, SEQ ID NO:6.

XX Glutaminase; Aspergillus oryzae KBN616; glutamic acid synthesis;
 KW fermentation; foodstuff production; miso; soy sauce;
 KW V8 protease digestion.
 XX
 OS Aspergillus oryzae.

XX JP2000166547-A.
 XX 20-JUN-2000.
 XX 07-DEC-1998; 98JP-00347127.
 XX 07-DEC-1998; 98JP-00347127.
 XX (AICH-) AICHI KEN PREFECTURE.
 PA (ICHI-) ICHIBIKI KK.
 XX
 DR WPI; 2000-477931/42.
 XX
 PT A new glutaminase and its preparation.
 XX
 PS Example 2; Page 9; 27pp; Japanese.

CC The invention relates to two novel glutaminases (AAB14781, AAB14782) from
 CC Aspergillus oryzae KBN616 and Aspergillus sojae BA-104 respectively which
 CC have molecular weights of approximately 73 kD (as determined by gel
 CC filtration). The enzymes have an optimum temperature of approximately 50
 CC degrees Celsius, and an optimum pH of about 8.5. The glutaminases
 CC catalyse the conversion of L-glutamine to L-glutamic acid, and may be
 CC used in the production of fermented foodstuffs such as soy sauce and
 CC miso. Sequences AAB14784-B14786 represent the N-terminal sequences
 CC determined for three V8 protease fragments (Pi-P3) of Aspergillus oryzae
 CC KBN616 Glutaminase in an exemplification of the invention
 XX
 SQ Sequence 12 AA;

Query Match 100.0%; Score 29; DB 3; Length 12;
 Best Local Similarity 100.0%; Pred. No. 6.5;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
 |||||
 Db 7 TYAMH 11

RESULT 4
 AAG65570
 ID AAG65570 standard; protein; 120 AA.
 XX
 AC AAG65570;
 XX
 DT 30-NOV-2001 (first entry)
 XX
 DE Amino acid sequence of protein seq Id No. 95.

XX Gene library; immunoglobulin; antibody library; human.
 KW
 XX

CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX
SQ Sequence 206 AA;

Query Match 100.0%; Score 29; DB 6; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0;

QY 1 TYAMH 5
Db 30 TYAMH 34
|||||

RESULT 8
ABO77482
ID ABO77482 standard; protein; 258 AA.
XX
XX ABO77482;
XX
XX 29-JUL-2004 (first entry)
XX
XX Pseudomonas aeruginosa polypeptide #9657.
XX
XX Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
XX
XX Pseudomonas aeruginosa.
XX
XX US6551795-B1.
XX
XX 22-APR-2003.
XX
XX 18-FEB-1999; 99US-00252991.
XX
XX 18-FEB-1998; 98US-0074788P.
XX
XX 27-JUL-1998; 98US-0094190P.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
XX
XX Rubenfield WJ, Nolling J, Deloughery C, Bush D;
XX
XX WPI; 2003-615309/58.
XX
XX N-PSDB; ABD11053.
XX
XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
XX useful as molecular targets for diagnostics, prophylaxis and treatment of
XX pathological conditions resulting from bacterial infection.
XX
XX Disclosure; SEQ ID NO 26228; 455pp; English.
XX
XX The invention relates to Pseudomonas aeruginosa polypeptides and the
XX polynucleotides encoding them. The sequences are useful in diagnosis and
XX therapy of pathological conditions, as molecular targets for diagnostics,
XX prophylaxis and treatment of pathological conditions resulting from a
XX bacterial infection, for evaluating a compound, such as a polypeptide,
XX for the ability to bind a *P. aeruginosa* nucleic acid, as components of
XX effective antibacterial targets, as targets for antibacterial drugs,
XX including anti-*P. aeruginosa* drugs, as templates for recombinant
XX production of *P. aeruginosa*-derived peptides or polypeptides, as target
XX components for diagnosis and/or treatment of *P. aeruginosa*-caused
XX infection, and in detection of *P. aeruginosa* sequences or other sequences
XX of Pseudomonas species using biochip technology. Sequences ABO67826-
XX ABO84396 represent *P. aeruginosa* polypeptides of the invention. Note: The
XX sequence data for this patent did not form part of the printed
XX specification but was obtained in electronic format from USPTO at
XX seqdata.uspto.gov/sequence.html
XX
XX Sequence 258 AA;
SQ

Best Local Similarity 100.0%; Pred. No. 77;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 32 TYAMH 36
|||||

RESULT 7
ABU24807
ID ABU24807 standard; protein; 206 AA.
XX
XX ABU24807;
XX
XX 19-JUN-2003 (first entry)
XX
XX Protein encoded by prokaryotic essential gene #10334.
XX
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
XX Clostridium botulinum.
XX
XX WO200277183-A2.
XX
XX 03-OCT-2002.
XX
XX 21-MAR-2002; 2002WO-US009107.
XX
XX 21-MAR-2001; 2001US-00815242.
XX
XX 06-SEP-2001; 2001US-00948993.
XX
XX 25-OCT-2001; 2001US-0342923P.
XX
XX 08-FEB-2002; 2002US-00072851.
XX
XX 06-MAR-2002; 2002US-0362699P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlson KL, Zyskind JW;
XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
XX WPI; 2003-029926/02.
XX
XX N-PSDB; ACA28677.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
XX for homologous nucleic acids required for cellular proliferation to
XX isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 25; SEQ ID NO 52731; 1766pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising any one of
XX the 6213 antisense sequences given in the specification where expression
XX of the nucleic acid inhibits proliferation of a cell. Also included are:
XX (1) a vector comprising a promoter operably linked to the nucleic acid
XX encoding a polypeptide whose expression is inhibited by the antisense
XX nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX polypeptide or its fragment whose expression is inhibited by the
XX antisense nucleic acid; (4) an antibody capable of specifically binding
XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
XX proliferation or the activity of a gene in an operon required for
XX proliferation; (7) identifying a compound that influences the activity of
XX the gene product or that has an activity against a biological pathway
XX required for proliferation, or that inhibits cellular proliferation; (8)
XX identifying a gene required for cellular proliferation or the biological
XX pathway in which a proliferation-required gene or its gene product lies
XX or a gene on which the test compound that inhibits proliferation of an
XX organism acts; (9) manufacturing an antibiotic; (10) profiling a
XX compound's activity; (11) a culture comprising strains in which the gene
XX product is overexpressed or underexpressed; (12) determining the extent
XX to which each of the strains is present in a culture or collection of
XX strains; or (13) identifying the target of a compound that inhibits the
XX proliferation of an organism. The antisense nucleic acids are useful for
XX identifying proteins or screening for homologous nucleic acids required
XX for cellular proliferation to isolate candidate molecules for rational
XX drug discovery programs, or for screening homologous nucleic acids

Query Match 100.0%; Score 29; DB 7; Length 258;
Best Local Similarity 100.0%; Pred. No. 1.6e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVAMH 5
Db 201 TVAMH 205

RESULT 9
ID ADN27332 standard; protein; 278 AA.
XX
AC ADN27332;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polypeptide #9985.
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
OS Bacteria.
XX
PN US2003233675-A1.
XX
PD 18-DEC-2003.
XX
PF 20-FEB-2003; 2003US-00369493.
XX
PR 21-FEB-2002; 2002US-0360039P.
XX
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX
DR WPI; 2004-061375/06.
XX
PT New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 9985; 122pp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan

CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 278 AA;

Query Match 100.0%; Score 29; DB 8; Length 278;
Best Local Similarity 100.0%; Pred. No. 1.7e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVAMH 5
Db 220 TVAMH 224

RESULT 10
AAG72483
ID AAG72483 standard; protein; 307 AA.
XX
AC AAG72483;
XX
DT 31-JUL-2001 (first entry)
XX
DE Human OR-like polypeptide query sequence, SEQ ID NO: 2164.
XX
KW Human; olfactory receptor; OR; primary scent determination;
KW secondary scent determination; polypeptide library; odour receptor;
KW scent profile; scent fingerprint; scent representation.
XX
OS Homo sapiens.
XX
PN WO200127159-A2.
XX
PD 19-APR-2001.
XX
PF 06-OCT-2000; 2000WO-US027592.
XX
PR 08-OCT-1999; 99US-0158615P.
PR 24-FEB-2000; 2000US-0184809P.
XX
PA (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
XX
DR WPI; 2001-290713/30.
XX
PT New polynucleotides which encode polypeptides involved in olfactory
PT sensation for identifying olfactory agonists and antagonists.
XX
PS Example 6; Page 1455-1456; 1857pp; English.
XX
CC The present sequence is a polypeptide encoded by one of 344 newly mined
CC human genes. It was used as a query sequence in a database search of
CC olfactory receptor (OR)-like sequences. The invention relates to isolated
CC polynucleotides encoding polypeptides involved in olfactory sensation.
CC The polynucleotides can be used in screening for olfactory agonists and
CC antagonists. The methods allow for the determination of primary scents
CC and the identification of the odour receptors used to detect these
CC primary scents. The methods also enable determination of secondary scents
CC and the identification of combinations of odour receptors that are
CC involved in detecting such secondary scents. This enables the
CC construction of a scent representation (also called a scent fingerprint
CC or scent profile), which may be used to re-create and edit scents.
CC Libraries of olfactory receptors are useful for determining the
CC interaction pattern of a composition with the receptors, and can be used
CC for determining differences in the olfactory faculties of different
CC individuals
XX
SQ Sequence 307 AA;

Query Match 100.0%; Score 29; DB 4; Length 307;

AC AAY50844;
 XX 24-FEB-2000 (first entry)
 DT DE A. oryzae glutaminase protein #2.
 XX
 XX Glutaminase; decomposition; glutamine; glutamic acid; ammonia;
 KW taste enhancer; seasoning; sauce; paste.
 XX
 XX Aspergillus oryzae.
 OS
 XX Key Location/Qualifiers
 FH Peptide 1..20
 FT /label= signal_peptide
 FT Protein 21..690
 XX
 XX WO9960104-A1.
 PN
 XX 25-NOV-1999.
 PD
 XX 12-MAY-1999; 99WO-JP002455.
 PF
 XX 15-MAY-1998; 98JP-00134080.
 PR 11-SEP-1998; 98JP-00258974.
 PR 14-OCT-1998; 98JP-00292443.
 PR 30-MAR-1999; 99JP-00089157.
 XX
 XX (AJIN) AJINOMOTO CO INC.
 PA
 XX Koibuchi K, Nagasaki H, Yuasa A, Kataoka J, Kitamoto K;
 PI
 XX WPI; 2000-053292/04.
 DR N-PSDB; AAZ43684.
 DR
 XX Aspergillus oryzae-originated glutaminase and partial amino-acid
 PT sequences for enhancing taste particularly in glutamic acid-converting
 PT food processing to make e.g. seasoning sauces and pastes.
 PT
 XX Example 3; Page 52-55; 74pp; Japanese.
 PS
 XX This invention describes a novel glutaminase enzyme isolated from
 CC Aspergillus oryzae which catalyses the decomposition of glutamine to
 CC glutamic acid and ammonia. The purified glutaminase and determined
 CC partial amino-acid sequence can be used for enhancing taste particularly
 CC in glutamic acid-converting food processing to give e.g. seasoning sauces
 CC and pastes as well as other seasoning materials. The gene thus obtained
 CC can be applied as probe for hybridization providing the gene-containing
 CC DNA fragments from genome and cDNA libraries of A. oryzae and A.
 CC nidulans, and subsequently modified glutaminase-producing breed. The
 CC novel strain of A. oryzae is a highly active because of its somatic
 CC secreting ability. This sequence represents the A. oryzae glutaminase
 CC enzyme described in the method of the invention
 XX
 SQ Sequence: 690 AA;
 Query Match 100.0%; Score 29; DB 3; Length 690;
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TYAMH 5
 Db 423 TYAMH 427
 RESULT 14
 ID AAY50835
 XX AAY50835 standard; protein; 690 AA.
 AC
 XX AAY50835;
 XX
 XX 24-FEB-2000 (first entry)
 DT
 XX A. oryzae glutaminase protein #1.
 DE

XX Glutaminase; decomposition; glutamine; glutamic acid; ammonia;
 KW taste enhancer; seasoning; sauce; paste.
 XX
 XX Aspergillus oryzae.
 OS
 XX Key Location/Qualifiers
 FH Peptide 1..20
 FT /label= signal_peptide
 FT Protein 21..690
 XX
 XX WO9960104-A1.
 PN
 XX 25-NOV-1999.
 PD
 XX 12-MAY-1999; 99WO-JP002455.
 PF
 XX 15-MAY-1998; 98JP-00134080.
 PR 11-SEP-1998; 98JP-00258974.
 PR 14-OCT-1998; 98JP-00292443.
 PR 30-MAR-1999; 99JP-00089157.
 XX
 XX (AJIN) AJINOMOTO CO INC.
 PA
 XX Koibuchi K, Nagasaki H, Yuasa A, Kataoka J, Kitamoto K;
 PI
 XX WPI; 2000-053292/04.
 DR N-PSDB; AAZ43677.
 DR
 XX Aspergillus oryzae-originated glutaminase and partial amino-acid
 PT sequences for enhancing taste particularly in glutamic acid-converting
 PT food processing to make e.g. seasoning sauces and pastes.
 PT
 XX Claim 1a; Page 41-44; 74pp; Japanese.
 PS
 XX This invention describes a novel glutaminase enzyme isolated from
 CC Aspergillus oryzae which catalyses the decomposition of glutamine to
 CC glutamic acid and ammonia. The purified glutaminase and determined
 CC partial amino-acid sequence can be used for enhancing taste particularly
 CC in glutamic acid-converting food processing to give e.g. seasoning sauces
 CC and pastes as well as other seasoning materials. The gene thus obtained
 CC can be applied as probe for hybridization providing the gene-containing
 CC DNA fragments from genome and cDNA libraries of A. oryzae and A.
 CC nidulans, and subsequently modified glutaminase-producing breed. The
 CC novel strain of A. oryzae is a highly active because of its somatic
 CC secreting ability. This sequence represents the A. oryzae glutaminase
 CC enzyme described in the method of the invention
 XX
 SQ Sequence: 690 AA;
 Query Match 100.0%; Score 29; DB 3; Length 690;
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TYAMH 5
 Db 423 TYAMH 427
 RESULT 15
 ID AAB14781
 XX AAB14781 standard; protein; 703 AA.
 AC
 XX AAB14781;
 XX
 XX 06-DEC-2000 (first entry)
 DT
 XX Aspergillus oryzae KBN616 glutaminase.
 DE
 XX Glutaminase; Aspergillus oryzae KBN616; glutamic acid synthesis;
 KW fermentation; foodstuff production; miso; soy sauce.
 XX
 XX Aspergillus oryzae.
 OS

XX Key Location/Qualifiers
FH Protein 34..703
FT /note= "Mature glutaminase; specifically claimed"
XX
PN JP2000166547-A.
XX
PD 20-JUN-2000.
XX
XX 07-DEC-1998; 98JP-00347127.
XX
XX 07-DEC-1998; 98JP-00347127.
XX
XX (AICH-) AICHI KEN PREFECTURE.
PA (ICHI-) ICHIBIKI KK.
XX
XX WPI; 2000-477931/42.
DR N-PSDB; AAA72204.
XX
PT A new glutaminase and its preparation.
XX
XX Claim 2; Page 15-17; 27pp; Japanese.
XX
XX This sequence represents a novel glutaminase from Aspergillus oryzae
CC K6N616. The invention relates to two novel glutaminases (AAB14781,
CC AAB14782) from Aspergillus oryzae K6N616 and Aspergillus sojae BA-104
CC respectively which have molecular weights of approximately 73 kD (as
CC determined by gel filtration). The enzymes have an optimum temperature of
CC approximately 50 degrees Celsius, and an optimum pH of about 8.5. The
CC glutaminases catalyze the conversion of L-glutamine to L-glutamic acid,
CC and may be used in the production of fermented foodstuffs such as soy
CC sauce and miso
XX
SQ Sequence 703 AA;

Query Match 100.0%; Score 29; DB 3; Length 703;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
|
|
|
|
Db 436 TYAMH 440

Search completed: October 14, 2005, 16:12:37
Job time : 42.4375 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2005, 16:00:04 ; Search time 9.84375 Seconds
(without alignments)
37.917 Million cell updates/sec

Title: US-10-614-959-10

Perfect score: 29

Sequence: 1 TYAMH 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.psp:**
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.psp:**
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.psp:**
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.psp:**
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.psp:**
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.psp:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	29	100.0	5	4	US-09-383-667-10
2	29	100.0	118	4	US-09-232-290-45
3	29	100.0	258	4	US-09-252-931A-26228
4	29	100.0	690	4	US-10-262-083-2
5	29	100.0	690	4	US-10-262-083-18
6	26	89.7	108	4	US-09-270-767-35497
7	26	89.7	108	4	US-09-270-767-50714
8	26	89.7	454	4	US-09-489-039A-10284
9	26	89.7	455	4	US-09-543-681A-8288
10	26	89.7	502	4	US-09-949-016-5992
11	26	89.7	507	4	US-09-949-016-7091
12	26	89.7	544	4	US-09-976-594-699
13	26	89.7	544	4	US-09-919-039-270
14	25	86.2	5	1	US-08-264-093-21
15	25	86.2	5	3	US-08-918-148-26
16	25	86.2	5	4	US-09-383-667-21
17	25	86.2	5	4	US-09-138-091A-26
18	25	86.2	5	4	US-09-424-840B-34
19	25	86.2	5	4	US-09-424-840B-91
20	25	86.2	5	4	US-09-830-748B-10
21	25	86.2	38	1	US-07-977-630-67
22	25	86.2	58	4	US-09-270-767-38850
23	25	86.2	58	4	US-09-270-767-54067
24	25	86.2	98	1	US-08-211-202-118
25	25	86.2	114	4	US-09-726-219A-222
26	25	86.2	116	1	US-08-211-202-141
27	25	86.2	117	3	US-08-545-809A-91

28	25	86.2	117	3	US-09-025-769B-24	Sequence 24, Appl
29	25	86.2	117	4	US-09-490-070A-24	Sequence 24, Appl
30	25	86.2	117	4	US-09-490-153-24	Sequence 24, Appl
31	25	86.2	117	4	US-09-490-324-24	Sequence 24, Appl
32	25	86.2	118	3	US-08-545-809A-145	Sequence 145, Appl
33	25	86.2	118	4	US-09-248-786A-14399	Sequence 14399, A
34	25	86.2	119	1	US-08-331-398A-46	Sequence 46, Appl
35	25	86.2	119	2	US-08-561-521-10	Sequence 10, Appl
36	25	86.2	119	2	US-08-561-521-12	Sequence 12, Appl
37	25	86.2	119	2	US-08-561-521-13	Sequence 13, Appl
38	25	86.2	119	2	US-08-331-397B-46	Sequence 46, Appl
39	25	86.2	119	2	US-08-759-804A-46	Sequence 46, Appl
40	25	86.2	119	3	US-09-227-693-46	Sequence 46, Appl
41	25	86.2	119	4	US-09-438-954-41	Sequence 41, Appl
42	25	86.2	119	5	PCT-US95-01219-10	Sequence 10, Appl
43	25	86.2	119	5	PCT-US95-01219-12	Sequence 12, Appl
44	25	86.2	119	5	PCT-US95-01219-13	Sequence 13, Appl
45	25	86.2	120	1	US-08-211-202-135	Sequence 135, Appl

ALIGNMENTS

RESULT 1

US-09-383-667-10
; Sequence 10, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camelia W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Eaton, Dan L.
; APPLICANT: Hass, Philip E.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Kirchhofer, Daniel
; APPLICANT: Suggett, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: P1661R2
; CURRENT APPLICATION NUMBER: US/09/383,667
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,233
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: US 60/122,767
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 10
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-667-10

Query Match 100.0%; Score 29; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
|
|
|
|
Db 1 TYAMH 5

RESULT 2

US-09-232-290-45
; Sequence 45, Application US/09232290A
; Patent No. 6815540
; GENERAL INFORMATION:
; APPLICANT: PLUCKTHUN, ANDREAS
; APPLICANT: NIEBA, LARS
; APPLICANT: HONEGGER, ANNEMARIE
; TITLE OF INVENTION: IMMUNOGLOBULIN SUPER FAMILY DOMAINS AND FRAGMENTS WITH
; FILE REFERENCE: MORPHO/7
; CURRENT APPLICATION NUMBER: US/09/232,290A
; CURRENT FILING DATE: 1999-01-15
; EARLIER APPLICATION NUMBER: PCT/EP96/02230

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; EARLIER FILING DATE: 1996-05-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Murine
US-09-232-290-45

Query Match          100.0%; Score 29; DB 4; Length 118;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TYAMH 5
Db      31 TYAMH 35

RESULT 3
US-09-252-991A-26228
; Sequence 26228, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26228
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26228

Query Match          100.0%; Score 29; DB 4; Length 258;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TYAMH 5
Db      201 TYAMH 205

RESULT 4
US-10-262-083-2
; Sequence 2, Application US/10262083
; Patent No. 6830905
; GENERAL INFORMATION:
; APPLICANT: KOIBUCHI, Kyoko
; APPLICANT: NAGASAKI, Hiroaki
; APPLICANT: YUASA, Ari
; APPLICANT: KATAOKA, Jiro
; APPLICANT: KITAMOTO, Katsuhiko
; TITLE OF INVENTION: A No. 6830905el Glutaminase, its Gene and a Method of Producing I
; FILE REFERENCE: 199438US-8222-10-0-PCT
; CURRENT APPLICATION NUMBER: US/10/262,083
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US/09/674,507
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: JP 10/134080
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: JP 10/258974
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: JP 10/292443
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: JP 11/89157
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
US-10-262-083-18

Query Match          100.0%; Score 29; DB 4; Length 690;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TYAMH 5
Db      423 TYAMH 427

RESULT 5
US-10-262-083-18
; Sequence 18, Application US/10262083
; Patent No. 6830905
; GENERAL INFORMATION:
; APPLICANT: KOIBUCHI, Kyoko
; APPLICANT: NAGASAKI, Hiroaki
; APPLICANT: YUASA, Ari
; APPLICANT: KATAOKA, Jiro
; APPLICANT: KITAMOTO, Katsuhiko
; TITLE OF INVENTION: A No. 6830905el Glutaminase, its Gene and a Method of Producing It
; FILE REFERENCE: 199438US-8222-10-0-PCT
; CURRENT APPLICATION NUMBER: US/10/262,083
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US/09/674,507
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: JP 10/134080
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: JP 10/258974
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: JP 10/292443
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: JP 11/89157
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
US-10-262-083-18

Query Match          100.0%; Score 29; DB 4; Length 690;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TYAMH 5
Db      423 TYAMH 427

RESULT 6
US-09-270-767-35497
; Sequence 35497, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
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; PRIOR APPLICATION NUMBER: PCT/JP99/02455
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
US-10-262-083-2

Query Match          100.0%; Score 29; DB 4; Length 690;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TYAMH 5
Db      423 TYAMH 427

RESULT 5
US-10-262-083-18
; Sequence 18, Application US/10262083
; Patent No. 6830905
; GENERAL INFORMATION:
; APPLICANT: KOIBUCHI, Kyoko
; APPLICANT: NAGASAKI, Hiroaki
; APPLICANT: YUASA, Ari
; APPLICANT: KATAOKA, Jiro
; APPLICANT: KITAMOTO, Katsuhiko
; TITLE OF INVENTION: A No. 6830905el Glutaminase, its Gene and a Method of Producing It
; FILE REFERENCE: 199438US-8222-10-0-PCT
; CURRENT APPLICATION NUMBER: US/10/262,083
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US/09/674,507
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: JP 10/134080
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: JP 10/258974
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: JP 10/292443
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: JP 11/89157
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
US-10-262-083-18

Query Match          100.0%; Score 29; DB 4; Length 690;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TYAMH 5
Db      423 TYAMH 427

RESULT 6
US-09-270-767-35497
; Sequence 35497, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
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SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35497
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-35497

Query Match 89.7%; Score 26; DB 4; Length 108;
Best Local Similarity 80.0%; Pred. No. 85;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
|||:
Db 64 TYALH 68

RESULT 7
US-09-270-767-50714
; Sequence 50714, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50714
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-50714

Query Match 89.7%; Score 26; DB 4; Length 108;
Best Local Similarity 80.0%; Pred. No. 85;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
|||:
Db 64 TYALH 68

RESULT 8
US-09-489-039A-10284
; Sequence 10284, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10284
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10284

Query Match 89.7%; Score 26; DB 4; Length 454;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
|||:
Db 64 TYALH 68

Db 152 TYALH 156

RESULT 9
US-09-543-681A-8288
; Sequence 8288, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 8288
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-8288

Query Match 89.7%; Score 26; DB 4; Length 455;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
|||:
Db 225 TYALH 229

RESULT 10
US-09-949-016-5992
; Sequence 5992, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5992
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-5992

Query Match 89.7%; Score 26; DB 4; Length 502;
Best Local Similarity 80.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
|||:
Db 398 TYALH 402

RESULT 11
US-09-949-016-7091
; Sequence 7091, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

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; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7091
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-7091

Query Match      89.7%; Score 26; DB 4; Length 507;
Best Local Similarity 80.0%; Pred.No. 4e+02; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 0;

Qy      1 TYAMH 5
Db      403 TYALH 407

RESULT 12
US-09-976-594-699
; Sequence 699, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 699
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 4113161CD1
US-09-976-594-699

Query Match      89.7%; Score 26; DB 4; Length 544;
Best Local Similarity 80.0%; Pred.No. 4.3e+02; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 0;

Qy      1 TYAMH 5
Db      485 TYALH 489

RESULT 13
US-09-919-039-270
; Sequence 270, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
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; SOFTWARE: PERL Program
; SEQ ID NO 270
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6727066 4113161CD1
US-09-919-039-270

Query Match      89.7%; Score 26; DB 4; Length 544;
Best Local Similarity 80.0%; Pred.No. 4.3e+02; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 0;

Qy      1 TYAMH 5
Db      485 TYALH 489

RESULT 14
US-08-264-093-21
; Sequence 21, Application US/08264093
; Patent No. 5639863
; GENERAL INFORMATION:
; APPLICANT: Michael D. Dan
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
; TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
; TITLE OF INVENTION: ANTIGEN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ridout & Maybee
; STREET: 2300 Richmond-Adelaide Centre
; STREET: 101 Richmond Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 2J7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS-DOS 6.00
; SOFTWARE: ASCII Editor
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/264,093
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA: No. 5639863 applicable
; ATTORNEY/AGENT INFORMATION:
; NAME: Lake, James R.
; REGISTRATION NUMBER: 31081
; REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 868-1482
; TELEFAX: (416) 362-0823
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: not applicable
; TOPOLOGY: linear
; US-08-264-093-21

Query Match      86.2%; Score 25; DB 1; Length 5;
Best Local Similarity 80.0%; Pred.No. 4.1e+05; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 0;

Qy      1 TYAMH 5
Db      1 SYAMH 5

RESULT 15
US-08-918-148-26
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; Sequence 26, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: P0979
; CURRENT APPLICATION NUMBER: US/08/918,148A
; CURRENT FILING DATE: 1997-08-25
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 26
; LENGTH: 5
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; NAME/KEY: 10D10scFv, 12B5scFv VH CDR1
; LOCATION: 1-5
; OTHER INFORMATION:
US-08-918-148-26

Query Match 86.2%; Score 25; DB 3; Length 5;
Best Local Similarity 80.0%; Pred. NO. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 1 TYGMH 5

Search completed: October 14, 2005, 16:22:00
Job time : 10.8438 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2005, 16:20:10 ; Search time 35.5469 Seconds
(without alignments)
58.615 Million cell updates/sec

Title: US-10-614-959-10
Perfect score: 29
Sequence: 1 TYAMH 5

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Gapop 10.0 , Gapext 0.5

Searched: 1859788 seqs, 416717961 residues

Total number of hits satisfying chosen parameters: 1859788

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:
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19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	5	18	US-10-989-462-64
2	29	100.0	11	15	US-10-468-543-91
3	29	100.0	119	20	US-11-003-819-12
4	29	100.0	121	16	US-10-466-242-25
5	29	100.0	123	18	US-10-989-462-7
6	29	100.0	128	16	US-10-466-242-47
7	29	100.0	137	16	US-10-425-115-311733
8	29	100.0	151	15	US-10-424-599-231272
9	29	100.0	158	16	US-10-425-115-211694
10	29	100.0	206	15	US-10-282-122A-52731
11	29	100.0	257	18	US-10-989-462-34

12 29 100.0 278 15 US-10-369-493-9985 Sequence 9985, Ap
13 29 100.0 690 14 US-10-262-083-2 Sequence 2, Appli
14 29 100.0 690 14 US-10-262-083-18 Sequence 18, Appli
15 29 100.0 690 16 US-10-851-337-2 Sequence 2, Appli
16 29 100.0 690 15 US-10-851-337-18 Sequence 18, Appli
17 26 89.7 11 15 US-10-468-543-35 Sequence 35, Appli
18 26 89.7 35 16 US-10-425-115-254835 Sequence 254835,
19 26 89.7 51 16 US-10-425-115-188939 Sequence 188939,
20 26 89.7 52 16 US-10-425-115-363604 Sequence 363604,
21 26 89.7 59 15 US-10-424-599-217913 Sequence 217913,
22 26 89.7 60 15 US-10-424-599-188252 Sequence 188252,
23 26 89.7 61 16 US-10-437-963-109084 Sequence 109084,
24 26 89.7 64 16 US-10-425-115-248574 Sequence 248574,
25 26 89.7 67 9 US-09-864-761-44407 Sequence 44407, A
26 26 89.7 67 15 US-10-424-599-190876 Sequence 190876,
27 26 89.7 69 16 US-10-425-115-271914 Sequence 271914,
28 26 89.7 73 15 US-10-424-599-192746 Sequence 192746,
29 26 89.7 73 15 US-10-424-599-205833 Sequence 205833,
30 26 89.7 77 15 US-10-424-599-245586 Sequence 245586,
31 26 89.7 79 9 US-09-764-846-193 Sequence 193, App
32 26 89.7 79 14 US-10-091-483-193 Sequence 193, App
33 26 89.7 85 16 US-10-767-701-48571 Sequence 48571, A
34 26 89.7 98 15 US-10-424-599-214193 Sequence 214193,
35 26 89.7 103 16 US-10-425-115-268350 Sequence 268350,
36 26 89.7 137 15 US-10-424-599-227653 Sequence 227653,
37 26 89.7 141 15 US-10-424-599-143644 Sequence 143644,
38 26 89.7 168 16 US-10-767-701-39988 Sequence 39988, A
39 26 89.7 221 15 US-10-094-749-2980 Sequence 2980, Ap
40 26 89.7 238 10 US-09-880-748-2053 Sequence 2053, Ap
41 26 89.7 238 15 US-10-293-418-2053 Sequence 2053, Ap
42 26 89.7 304 15 US-10-282-122A-45565 Sequence 45565, A
43 26 89.7 355 17 US-10-831-070-42 Sequence 42, Appli
44 26 89.7 370 9 US-09-738-626-3768 Sequence 3768, Ap
45 26 89.7 370 9 US-09-738-626-5177 Sequence 5177, Ap

ALIGNMENTS

RESULT 1
US-10-989-462-64
; Sequence 64, Application US/10989462
; Publication No. US20050220795A1
; GENERAL INFORMATION:
; APPLICANT: Wittup, K. Dane
; APPLICANT: Yeung, Yik Andy
; TITLE OF INVENTION: ANTI-HYDROXYLASE ANTIBODIES AND USES
; FILE REFERENCE: 01997-329001
; CURRENT APPLICATION NUMBER: US/10/989,462
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/520,114
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US 60/563,514
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-989-462-64

Query Match 100.0%; Score 29; DB 18; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
DB 1 TYAMH 5

```

; Sequence 25, Application US/10466242
; Publication No. US20040208887A1
; GENERAL INFORMATION:
; APPLICANT: Drakenberg, Katarina
; APPLICANT: Persson, Mats
; TITLE OF INVENTION: Materials and methods for treatment of hepatitis C
; FILE REFERENCE: 0380-P03248US00
; CURRENT APPLICATION NUMBER: US/10/466,242
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/SE02/00044
; PRIOR FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(121)
; OTHER INFORMATION: Clone 2a:14 VH
US-10-466-242-25

Query Match      100.0%; Score 29; DB 16; Length 121;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 33 TYAMH 37

RESULT 5
US-10-989-462-7
; Sequence 7, Application US/10989462
; Publication No. US20050220795A1
; GENERAL INFORMATION:
; APPLICANT: Wittrup, K. Dane
; APPLICANT: Yeung, Yik Andy
; TITLE OF INVENTION: ANTI-HYDROXYLASE ANTIBODIES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 01997-329001
; CURRENT APPLICATION NUMBER: US/10/989,462
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/520,114
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US 60/563,514
; PRIOR FILING DATE: 2004-04-19
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-989-462-7

Query Match      100.0%; Score 29; DB 18; Length 123;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 31 TYAMH 35

RESULT 6
US-10-466-242-47
; Sequence 47, Application US/10466242
; Publication No. US20040208887A1
; GENERAL INFORMATION:
; APPLICANT: Drakenberg, Katarina
; APPLICANT: Persson, Mats
; TITLE OF INVENTION: Materials and methods for treatment of hepatitis C
; FILE REFERENCE: 0380-P03248US00
; CURRENT APPLICATION NUMBER: US/10/466,242
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/SE02/00044
; PRIOR FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(121)
; OTHER INFORMATION: Clone 2a:14 VH
US-10-466-242-25

Query Match      100.0%; Score 29; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 2 TYAMH 6

RESULT 3
US-11-003-819-12
; Sequence 12, Application US/11003819
; Publication No. US20050158323A1
; GENERAL INFORMATION:
; APPLICANT: Evans, Elizabeth E.
; APPLICANT: Paris, Mark J.
; APPLICANT: Sabarwal, Deepak M.
; APPLICANT: Zauderer, Maurice
; APPLICANT: Smith, Ernest S.
; TITLE OF INVENTION: Methods of Killing Tumor Cells by Targeting Internal Antigens
; TITLE OF INVENTION: Exposed on Apoptotic Tumor Cells
; FILE REFERENCE: 1843.0190002
; CURRENT APPLICATION NUMBER: US/11/003,819
; CURRENT FILING DATE: 2004-12-05
; PRIOR APPLICATION NUMBER: US 60/256,572
; PRIOR FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: US 60/531,688
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-003-819-12

Query Match      100.0%; Score 29; DB 20; Length 119;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 31 TYAMH 35

RESULT 4
US-10-466-242-25
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APPLICANT: Persson, Mats
; TITLE OF INVENTION: Materials and methods for treatment of hepatitis C
; FILE REFERENCE: 0380-P03248US00
; CURRENT APPLICATION NUMBER: US/10/466,242
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/SE02/00044
; PRIOR FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(128)
; OTHER INFORMATION: Clone 2b:5 VH
US-10-466-242-47

Query Match 100.0%; Score 29; DB 16; Length 128;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 32 TYAMH 36

RESULT 7
US-10-425-115-311733
; Sequence 311733, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 311733
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_47353C.1.psp
US-10-425-115-311733

Query Match 100.0%; Score 29; DB 16; Length 137;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 16 TYAMH 20

RESULT 8
US-10-424-599-231272
; Sequence 231272, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 231272
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(151)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_50860C.1.psp
US-10-424-599-231272

Query Match 100.0%; Score 29; DB 15; Length 151;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 120 TYAMH 124

RESULT 9
US-10-425-115-211694
; Sequence 211694, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 211694
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(158)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_124664C.1.psp
US-10-425-115-211694

Query Match 100.0%; Score 29; DB 16; Length 158;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 56 TYAMH 60

RESULT 10
US-10-282-122A-52731
; Sequence 52731, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangou
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant

APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 52731
LENGTH: 206
TYPE: PRT
ORGANISM: Clostridium botulinum
US-10-282-122A-52731

Query Match 100.0%; Score 29; DB 15; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 30 TYAMH 34

RESULT 11
US-10-989-462-34
Sequence 34, Application US/10989462
Publication No. US20050220795A1
GENERAL INFORMATION:
APPLICANT: Wittrup, K. Dane
APPLICANT: Yeung, Yik Andy
TITLE OF INVENTION: ANTI-HYDROXYLASE ANTIBODIES AND USES
FILE REFERENCE: 01997-329001
CURRENT APPLICATION NUMBER: US/10/989,462
CURRENT FILING DATE: 2004-11-15
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: US 60/520,114
PRIOR FILING DATE: 2004-04-19
NUMBER OF SEQ ID NOS: 319
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 34
LENGTH: 257
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetically generated peptide
US-10-989-462-34

Query Match 100.0%; Score 29; DB 18; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 31 TYAMH 35

RESULT 12
US-10-369-493-9985
Sequence 9985, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 9985
LENGTH: 278
TYPE: PRT
ORGANISM: magnetite-containing magnetic coccus
US-10-369-493-9985

Query Match 100.0%; Score 29; DB 15; Length 278;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 220 TYAMH 224

RESULT 13
US-10-262-083-2
Sequence 2, Application US/10262083
Publication No. US20030170670A1
GENERAL INFORMATION:
APPLICANT: KOIBUCHI, Kyoko
APPLICANT: NAGASAKI, Hiroaki
APPLICANT: YUASA, Aki
APPLICANT: KITAMOTO, Katsuhiko
TITLE OF INVENTION: A NO. US20030170670A1el Glutaminase, its Gene and a Method of Proc
FILE REFERENCE: 199438US-8222-10-0-PCT
CURRENT APPLICATION NUMBER: US/10/262,083
CURRENT FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: US/09/674,507
PRIOR FILING DATE: 2000-11-15
PRIOR APPLICATION NUMBER: JP 10/134080
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: JP 10/258974
PRIOR FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: JP 10/292443
PRIOR FILING DATE: 1998-10-14
PRIOR APPLICATION NUMBER: JP 11/89157
PRIOR FILING DATE: 1999-03-30
PRIOR APPLICATION NUMBER: PCT/JP99/02455
PRIOR FILING DATE: 1999-05-12
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 690
TYPE: PRT
ORGANISM: Aspergillus oryzae
US-10-262-083-2

Query Match 100.0%; Score 29; DB 14; Length 690;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 423 TYAMH 427

RESULT 14
US-10-262-083-18
; Sequence 18, Application US/10262083
; Publication No. US20030170670A1
; GENERAL INFORMATION:
; APPLICANT: KOIBUCHI, Kyoko
; APPLICANT: NAGASAKI, Hiroaki
; APPLICANT: YUASA, Aki
; APPLICANT: KATAOKA, Jiro
; APPLICANT: KITAMOTO, Katsuhiko
; TITLE OF INVENTION: A No. US20030170670A1el Glutaminase, its Gene and a Method of Pro
; FILE REFERENCE: 199438US-8222-10-0-PCT
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US/10/262,083
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US/09/674,507
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: JP 10/134080
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: JP 10/258974
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: JP 10/292443
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: JP 11/89157
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: PCT/JP99/02455
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
US-10-262-083-18

Query Match 100.0%; Score 29; DB 14; Length 690;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 423 TYAMH 427

RESULT 15
US-10-851-337-2
; Sequence 2, Application US/10851337
; Publication No. US20040229322A1
; GENERAL INFORMATION:
; APPLICANT: KOIBUCHI, Kyoko
; APPLICANT: NAGASAKI, Hiroaki
; APPLICANT: YUASA, Aki
; APPLICANT: KATAOKA, Jiro
; APPLICANT: KITAMOTO, Katsuhiko
; TITLE OF INVENTION: A Novel Glutaminase, its Gene and a Method of
; FILE REFERENCE: 199438US-8222-10-0-PCT
; CURRENT FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US/10/262,083
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US/09/674,507
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: JP 10/134080

; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: JP 10/258974
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: JP 10/292443
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: JP 11/89157
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: PCT/JP99/02455
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
US-10-851-337-2

Query Match 100.0%; Score 29; DB 16; Length 690;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 423 TYAMH 427

Search completed: October 14, 2005, 17:00:41
Job time : 36.5469 secs

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A:Title: Immunoglobulin D switching can occur through homologous recombination in human
A:Reference number: A35676; MUID:90287160; PMID:2113175
A:Accession: A35676
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-138 <WHI>
A:Cross-references: GB:M38066; NID:9185466; PID:AAA52974.1; PID:9553407
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F34-117/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 29; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 50 TYAMH 54
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RESULT 3
D71184
adenylate kinase (EC 2.7.4.3) PH1753 [similarity] - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C:Accession: D71184
R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: D71184
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-196 <KAW>
A:Cross-references: UNIPROT:O59443; GB:AP000007; NID:g3236134; PIDN:BAA30867.1; PID:g325
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH1753
C:Keywords: phosphotransferase

Query Match 100.0%; Score 29; DB 2; Length 196;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 157 TYAMH 161
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RESULT 4
B83290
conserved hypothetical protein PA2847 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: B83290
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: B83290
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-249 <STO>
A:Cross-references: UNIPROT:Q9HZZ6; GB:AE004711; GB:AE004091; NID:g9948927; PIDN:AAG0623
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA2847

Query Match 100.0%; Score 29; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 192 TYAMH 196
|||||
RESULT 5
H71347

hypothetical protein TP0245 - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C:Accession: H71347
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDo
rsey, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A71250; MUID:98332770; PMID:9665876
A:Accession: H71347
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1151 <COL>
A:Cross-references: UNIPROT:O83273; GB:AE001206; GB:AE000520; NID:g3322514; PIDN:AAC65523;
A:Experimental source: strain Nichols
C:Genetics:
A:Gene: TP0245
C:Superfamily: syphilis spirochete hypothetical protein TP0245

Query Match 100.0%; Score 29; DB 2; Length 1151;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 700 TYAMH 704
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RESULT 6
I54632
tsh protein - Escherichia coli
C:Species: Escherichia coli
C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C:Accession: I54632
R;Provence, D.L.; Curtiss, R.
Infect. Immun. 62, 1369-1380, 1994
A:Title: Isolation and characterization of a gene involved in hemagglutination by an avia
A:Reference number: I54632; MUID:94178945; PMID:8132344
A:Accession: I54632
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1377 <RES>
A:Cross-references: UNIPROT:Q47692; GB:L27423; NID:g469235; PIDN:AAA24698.1; PID:g469236
C:Superfamily: IGA-specific metalloendopeptidase

Query Match 100.0%; Score 29; DB 2; Length 1377;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 341 TYAMH 345
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RESULT 7
T34500
hypothetical protein ZK1248.17 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T34500
R;Latreille, P.
submitted to the EMBL Data Library, June 1995
A:Description: The sequence of C. elegans cosmid ZK1248.
A:Reference number: Z21534
A:Accession: T34500
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-95 <LAT>
A:Cross-references: UNIPROT:Q23428; EMBL:U29244; PIDN:U29244; GSPDB:GN000020; CESP:ZK1
A:Experimental source: strain Bristol N2; clone ZK1248
C:Genetics:
A:Gene: CESP:ZK1248.17

A;Map position: 2
C;Superfamily: Caenorhabditis elegans major sperm protein

Query Match 89.7%; Score 26; DB 2; Length 95;
Best Local Similarity 80.0%; Pred. No. 32;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
DB 12 TVSMH 16

RESULT 8
I50675
retinol-binding protein precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50675; S42887
R;Vieira, A.V.; Kuchler, K.; Schneider, W.J.
DNA Cell Biol. 14, 403-410, 1995
A;Title: Retinol in avian oogenesis: molecular properties of the carrier protein.
A;Reference number: I50675; MUID:95267350; PMID:7748490
A;Accession: I50675
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-196 <VIE>
A;Cross-references: UNIPROT:P41263; EMBL:X77960; NID:G457778; PIDN:CAA54922.1; PID:G457778
C;Genetics:
A;Gene: RBP
C;Superfamily: lipocalin; lipocalin homology
F;1-21/Domain: signal sequence #status predicted <SIG>
F;36-195/Domain: lipocalin homology <LIP>
F;25-181,91-195,141-150/disulfide bonds: #status predicted

Query Match 89.7%; Score 26; DB 2; Length 196;
Best Local Similarity 80.0%; Pred. No. 67;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
DB 134 TYALH 138

RESULT 9
H86403
hypothetical protein F28L5.12 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: H86403
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Xu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: H86403
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-213 <STO>
A;Cross-references: UNIPROT:Q9C6N1; GB:A8005172; NID:g10998924; PIDN:AAG26064.1; GSPDB:G
C;Genetics:
A;Map position: 1

Query Match 89.7%; Score 26; DB 2; Length 213;
Best Local Similarity 80.0%; Pred. No. 73;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5

DB 202 TYALH 206

RESULT 10
E90215
conserved hypothetical protein [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: E90215
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-v
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arrett, R.A.; Ragan, M.A.; Sengen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: E90215
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-222 <KUR>
A;Cross-references: UNIPROT:Q9UX67; GB:AE006641; NID:gl3813846; PIDN:AAK40980.1; GSPDB:G
C;Genetics:
A;Gene: SSO0678
C;Superfamily: hypothetical protein MJ0570

Query Match 89.7%; Score 26; DB 2; Length 222;
Best Local Similarity 80.0%; Pred. No. 76;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
DB 14 TYALH 18

RESULT 11
T22924
hypothetical protein F5856.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22924
R;McMurray, A.
submitted to the EMBL Data Library, April 1996
A;Reference number: Z19638
A;Accession: T22924
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-228 <WIL>
A;Cross-references: UNIPROT:Q20984; EMBL:Z70754; PIDN:CAA94778.1; GSPDB:GN00023; CESP:F5
A;Experimental source: clone F58E6
C;Genetics:
A;Gene: CESP:F58E6.8
A;Map position: 5
A;Introns: 153/2
C;Superfamily: Caenorhabditis elegans hypothetical protein Y75B12A.2

Query Match 89.7%; Score 26; DB 2; Length 228;
Best Local Similarity 80.0%; Pred. No. 78;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
DB 177 TYALH 181

RESULT 12
AD1165
B. subtilis YvpB protein homolog lmo0724 [imported] - Listeria monocytogenes (strain EGD-
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AD1165
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.;
D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of *Listeria* species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AD1165
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-242 <GLA>
A;Cross-references: UNIPROT:Q8Y918; GB:NC_003210; PIDN:CAC98902.1; PID:g16410113; GSPDB:
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo0724
C;Superfamily: Bacillus subtilis hypothetical protein yvpB

Query Match 89.7%; Score 26; DB 2; Length 242;
Best Local Similarity 80.0%; Pred. No. 83;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
|||:
191 TYSMH 195

Db

RESULT 13
AD1524
B. subtilis YvpB protein homolog lin0732 [imported] - *Listeria innocua* (strain Clip11262
C;Species: *Listeria innocua*
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AD1524
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duseurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of *Listeria* species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AD1524
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-242 <GLA>
A;Cross-references: UNIPROT:Q92DT0; GB:AL592022; PIDN:CAC95964.1; PID:g16413184; GSPDB:C
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin0732
C;Superfamily: Bacillus subtilis hypothetical protein yvpB

Query Match 89.7%; Score 26; DB 2; Length 242;
Best Local Similarity 80.0%; Pred. No. 83;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
|||:
191 TYSMH 195

Db

RESULT 14
A29487
cytochrome P450 3A6 (version 1) - rabbit
N;Alternate names: cytochrome P450 3c
N;Contains: oxidoreductase (EC 1.-.-.-)
C;Species: *Oryctolagus cuniculus* (domestic rabbit)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: A29487
R;Dalet, C.; Clair, P.; Daujat, M.; Fort, P.; Blanchard, J.M.; Maurel, P.
DNA 7, 39-46, 1988
A;Title: Complete sequence of cytochrome P450 3c cDNA and presence of two mRNA species w
A;Reference number: A29487; MUID:88166352; PMID:3349903
A;Accession: A29487
A;Molecule type: mRNA
A;Residues: 1-501 <DAL>
A;Cross-references: UNIPROT:P11707; GB:M19139; NID:g165573; PIDN:AAA31430.1; PID:g165574

C;Genetics:
A;Gene: CYP3A6
C;Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C;Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; monooxygenase;
F;301-462/Domain: cytochrome P450 homology <P45>
F;440/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 89.7%; Score 26; DB 2; Length 501;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
|||:
396 TYALH 400

Db

RESULT 15
A34236
cytochrome P450 3A6 (version 2) - rabbit
N;Alternate names: cytochrome P450 3c
N;Contains: oxidoreductase (EC 1.-.-.-)
C;Species: *Oryctolagus cuniculus* (domestic rabbit)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: A34236
R;Potenza, C.L.; Pendurthi, U.R.; Strom, D.K.; Tukey, R.H.; Griffin, K.J.; Schwab, G.E.;
J. Biol. Chem. 264, 16222-16228, 1989
A;Title: Regulation of the rabbit cytochrome P-450 3c gene. Age-dependent expression and
A;Reference number: A34236; MUID:89380226; PMID:2777787
A;Accession: A34236
A;Molecule type: mRNA
A;Residues: 1-501 <POT>
A;Cross-references: UNIPROT:P11707; GB:J05034; NID:g164829; PIDN:AAA31178.1; PID:g164830
C;Genetics:
A;Gene: CYP3A6
C;Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C;Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; monooxygenase;
F;300-462/Domain: cytochrome P450 homology <P45>
F;440/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 89.7%; Score 26; DB 2; Length 501;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
|||:
396 TYALH 400

Db

Search completed: October 14, 2005, 16:23:35
Job time : 7.95312 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2005, 15:51.44 ; Search time 33.2812 Seconds
(without alignment)
76.932 Million cell updates/sec

Title: US-10-614-959-10
Perfect score: 29
Sequence: 1 TYAMH 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	29	100.0	72	2	Q8RZ81	Q8RZ81	oryza sativ
2	29	100.0	122	1	HV3H_HUMAN	P01769	homo sapien
3	29	100.0	158	2	Q8PKV7	Q8PKV7	xanthomonas
4	29	100.0	196	1	KADA_PYRO	Q8K4V3	pyrococcus
5	29	100.0	249	2	Q9HZZ6	Q9HZZ6	pseudomonas
6	29	100.0	356	2	Q962C9	Q962C9	podocoryne
7	29	100.0	481	2	Q6N097	Q6N097	homo sapien
8	29	100.0	493	2	Q68CN4	Q68CN4	homo sapien
9	29	100.0	531	2	Q23WR9	Q23WR9	escherichia
10	29	100.0	544	2	Q6AQ19	Q6AQ19	desulfotale
11	29	100.0	648	2	Q9V6J4	Q9V6J4	drosofila
12	29	100.0	690	2	Q9HGS1	Q9HGS1	aspergillus
13	29	100.0	690	2	Q9UVX9	Q9UVX9	aspergillus
14	29	100.0	747	1	V222_FOWPV	Q9J513	fovilpox vir
15	29	100.0	1151	1	Y245_TREPA	Q83273	treponema p
16	29	100.0	1377	2	Q88093	Q88093	escherichia
17	29	100.0	1377	2	Q47692	Q47692	escherichia
18	29	100.0	7488	2	Q6JHN6	Q6JHN6	saccharopol
19	26	89.7	65	2	Q62XJ3	Q62XJ3	bacillus li
20	26	89.7	95	2	Q23428	Q23428	caenorhabdi
21	26	89.7	108	2	Q6XNPF	Q6XNPF	hevea bras
22	26	89.7	138	2	Q7Z4A7	Q7Z4A7	pyrobaculum
23	26	89.7	160	2	Q72447	Q72447	homo sapien
24	26	89.7	169	2	Q66BK2	Q66BK2	yersinia ps
25	26	89.7	173	2	Q86SK1	Q86SK1	homo sapien
26	26	89.7	175	2	Q6LMV3	Q6LMV3	photobacter
27	26	89.7	187	2	Q67RR8	Q67RR8	symbiobacte
28	26	89.7	196	1	RETB_CHICK	P41263	gallus gall
29	26	89.7	202	2	Q9CKQ5	Q9CKQ5	pasteurella
30	26	89.7	213	2	Q9C6N1	Q9C6N1	arabidopsis
31	26	89.7	217	2	Q9DGG0	Q9DGG0	xenopus lae

32	26	89.7	222	2	Q9UX67	Q9UX67	sulfolobus
33	26	89.7	228	2	Q20984	Q20984	caenorhabdi
34	26	89.7	229	2	Q85HP4	Q85HP4	trichoderma
35	26	89.7	242	2	Q8Y918	Q8Y918	listeria in
36	26	89.7	242	2	Q92DT0	Q92DT0	listeria in
37	26	89.7	242	2	Q722H3	Q722H3	listeria mo
38	26	89.7	244	2	Q8WRC3	Q8WRC3	tetrahymena
39	26	89.7	248	2	Q885R2	Q885R2	pseudomonas
40	26	89.7	266	2	Q7Q8W1	Q7Q8W1	anopheles g
41	26	89.7	296	2	Q7QJU6	Q7QJU6	anopheles g
42	26	89.7	302	2	Q65M55	Q65M55	bacillus li
43	26	89.7	304	2	Q635I5	Q635I5	bacillus ce
44	26	89.7	304	2	Q711K1	Q711K1	bacillus ce
45	26	89.7	304	2	Q818Z0	Q818Z0	bacillus ce

ALIGNMENTS

RESULT 1

Q8RZ81	PRELIMINARY;	PRT;	72 AA.
AC Q8RZ81;			
DT 01-JUN-2002 (Tremblrel. 21, Created)			
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)			
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)			
DE Bi065G12.14 protein.			
GN Name=Bi065G12.14;			
OS Oryza sativa (japonica cultivar-group).			
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			
OC Ehrhartoideae; Oryzae; Oryza.			
OX NCBI_TaxID=39947;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX PubMed=12447438; DOI=10.1038/nature01184;			
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,			
RA Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,			
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,			
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,			
RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,			
RA Ikeno M., Itoh S., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,			
RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,			
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,			
RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,			
RA Namiki N., Negishi M., Ohta I., Ono N., Saiji S., Sakai, K., Shibata M.,			
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Teraawa K., Tsuji K.,			
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,			
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,			
RA Yano M., Jiang J., Gojobori T.;			
RT "The genome sequence and structure of rice chromosome 1.";			
RL Nature 420:312-316(2002).			
DR EMBL; AP003791; BAB90532.1; -.			
SQ Gramene: Q8RZ81; -.			
SQ SEQUENCE 72 AA; 7677 MW; 6A9368D674BE00A3 CRC64;			

Query Match 100.0%; Score 29; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 25 TYAMH 29

RESULT 2

HV3H_HUMAN	STANDARD;	PRT;	122 AA.
AC P01769;			
DT 21-JUL-1986 (Rel. 01, Created)			
DT 21-JUL-1986 (Rel. 01, Last sequence update)			
DT 05-JUL-2004 (Rel. 44, Last annotation update)			
DE Ig heavy chain V-III region GA.			

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=74175307; PubMed=4208843;
RA Florent G., Lehman D., Putnam F.W.;
RT "the switch point in mu heavy chains of human Igm immunoglobulins.";
RL Biochemistry 13:2482-2498(1974).
CC -|- MISCELLANEOUS: This chain was isolated from a Waldenström's
CC macroglobulin.
CC -|- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02052; M3HUGA.
DR HSP; P01772; 2FB4.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
DR PROSITE: PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region;
KW Pyridinolone carboxylic acid.
FT DOMAIN 1 112 Ig-like.
FT MOD_RES 1 122 Pyridinolone carboxylic acid.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13166 MW; 745586959E84100A CRC64;

Query Match 100.0%; Score 29; DB 1; Length 122;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 31 TYAMH 35

RESULT 3
Q8PKV7 PRELIMINARY; PRT; 158 AA.
ID Q8PKV7
AC Q8PKV7
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein XAC2050.
GN OrderedLocustNames=XAC2050;
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=22024217; PubMed=4174598; DOI=10.1038/4174598;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Canarotte G., Cannavan F., Cardoso J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Fornighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locati E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.P., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kiteajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities.";

RL Nature 417:459-463(2002).
DR EMBL: AE011840; AAC36912.1; -.
DR InterPro: IPR001412; tRNA-synt 1.
DR PROSITE: PS00178; AA_TRNA_LIGASE_1; UNKNOWN_1.
RW Complete proteome.
SQ SEQUENCE 158 AA; 17289 MW; C1B1FB23AA6E930B CRC64;

Query Match 100.0%; Score 29; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 132 TYAMH 136

RESULT 4
KADA PYRHO STANDARD; PRT; 196 AA.
ID KADA PYRHO
AC O59443;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).
GN Name=adka; OrderedLocustNames=PHI753;
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka K., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kishida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RNA Res. 5:55-76(1998).
CC -|- CATALYTIC ACTIVITY: ATP + AMP = 2 ADP.
CC -|- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).
CC -|- SIMILARITY: Belongs to the archaeal adenylate kinase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AP000007; BAA30867.1; -.
DR PIR: D71184; D71184.
DR HSP; P43410; 1K19.
DR HAMAP: MF_00234; -; 1.
KW ATP-binding; Complete proteome; Kinase; Transferase.
FT NP_BIND 9 17 ATP (Potential).
SQ SEQUENCE 196 AA; 22413 MW; 26C834ABE944D5F CRC64;

Query Match 100.0%; Score 29; DB 1; Length 196;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 157 TYAMH 161

RESULT 5
Q9H226

ID Q9H2Z6 PRELIMINARY; PRT; 249 AA.

AC Q9HZ26;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-JUN-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 24, Last annotation update)

DE Hypothetical protein

GN OrderedLocustNames=PA2847;

OS Pseudomonas aeruginosa.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

OC Pseudomonadaceae; Pseudomonas.

OX NCBI_TaxID=287;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 15692 / PAO1;

RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;

RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warriner P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";

RL Nature 406:959-964(2000).

DR EMBL; AB004711; AACG6235.1; -.

DR PIR; B83290; B83290.

DR InterPro; IPR002781; DUF81.

DR Pfam; PF01925; DUF81; 1.

KW Complete proteome; Hypothetical protein.

SQ SEQUENCE 249 AA; 25989 MW; 8B24827F50F64D6A CRC64;

Query Match 100.0%; Score 29; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 192 TYAMH 196
|||||

RESULT 6

Q962C9 PRELIMINARY; PRT; 356 AA.

AC Q962C9

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Transcription factor Cnox4-Pc.

OS Podocoryne carnea.

OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroids; Anthomedusae;

OC Hydractiniidae; Podocoryne.

OX NCBI_TaxID=6096;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=21349874; PubMed=11456446; DOI=10.1006/dbio.2001.0299;

RX Yanze N., Spring J., Schmidl C., Schmid V.; "Conservation of Hox/Parahox-related genes in the early development of a cnidarian.";

RL Dev. Biol. 236:89-98(2001).

RR 1- SUBCELLULAR LOCATION: Nuclear (By similarity).

DR EMBL; AY036893; AKG3185.1; -.

DR HSSP; P09089; 1K22.

DR GO; GO:0005634; C:nucleus; IEA.

DR GO; GO:0003700; F:transcription factor activity; IEA.

DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

DR InterPro; IPR001356; Homeobox.

DR InterPro; IPR009057; Homeodomain like.

DR InterPro; IPR000047; HTH lamrepresr.

DR Pfam; PF00046; Homeobox; 1.

DR PRINTS; PR00024; HOMEBOX.

DR PRINTS; PR00031; HTHREPRESSR.

DR SMART; SM00389; HOX; 1.

DR PROSITE; PS00027; HOMEBOX_1; 1.

DR PROSITE; PS00027; HOMEBOX_1; 1.

DR PROSITE; PS00027; HOMEBOX_1; 1.

RC TISSUE=Rectum tumor;
RG The German cDNA Consortium;
RA Bloecker H., Boecker M., Brandt P., Mewes H.W., Weil B., Amid C.,
OB Oanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: CR749861; CAH18705.1; -;
DR InterPro; IPR003599; Ig-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 493 AA; 54117 MW; A1E4F5ED3FA8AB40 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 493;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 73 TYAMH 77

RESULT 9
Q83WR9 ID Q83WR9 PRELIMINARY; PRT; 531 AA.
AC Q83WR9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Tsh protein (fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=APEC13;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY280856; AAP33781.1; -;
DR GO; GO:004222; P:serine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000710; Peptidase_S6.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF02395; IGAL; 1.
DR PRINTS; PR00921; IGASERPTASE.
FT NON_TER 531 531
SQ SEQUENCE 531 AA; 56485 MW; 60AC4E859A7AFC03 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 531;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 341 TYAMH 345

RESULT 10
Q6AQ19 ID Q6AQ19 PRELIMINARY; PRT; 544 AA.
AC Q6AQ19;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Probable acetyl-coenzyme A synthetase.
GN Name=acs; OrderedLocuNames=DP0825;
OS Desulfotalea psychrophila.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacteriales;
OC Desulfobulbaceae; Desulfotalea.
OX NCBI_TaxID=84980;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LSV54 / DSM 12343;
RX PubMed=15305914;
RA Babus R., Ruepp A., Frickey T., Rattei T., Fartmann B., Stark M.,
BA Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K.,
RA Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,
RA Klenk H.-P.;
RT "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
from permanently cold Arctic sediments.";
RL Environ. Microbiol. 6:1887-902(2004).
CC -|- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
family.
DR EMBL: CR522870; CAG35554.1; -;
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR000873; AMP-bind.
DR Pfam; PF00501; AMP-binding; 1.
DR PRINTS; PR00154; AMPBINDING.
DR PROSITE; PS00455; AMP_BINDING; 1.
KW Complete proteome.
SQ SEQUENCE 544 AA; 60412 MW; CAD62D99E4CCEBF7 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 544;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 307 TYAMH 311

RESULT 11
Q9V6J4 ID Q9V6J4 PRELIMINARY; PRT; 648 AA.
AC Q9V6J4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE CG3915-PB (GH27039p).
GN Name=Dri-2; ORFNames=CG3915;
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Balley R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brattier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.B., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RA "The genome sequence of Drosophila melanogaster";
RA Science 287:2185-2195(2000).
RL [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celnikier S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskaas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
RA "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RA melanogaster euchromatic genome sequence";
RA Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RL [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskaas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celnikier S.E.,
RA "The transposable elements of the Drosophila melanogaster euchromatin:
RA a genomics perspective";
RA Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RL [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celnikier S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.,
RA "Annotation of the Drosophila melanogaster euchromatic genome: a
RA systematic review";
RA Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RL [5]
RP SEQUENCE FROM N.A.
RX SEQUENCE FROM N.A.
RA FlyBase;
RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RL [6]
RP SEQUENCE FROM N.A.
RX SEQUENCE FROM N.A.
RA FlyBase;
RA Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RL [7]
RP SEQUENCE FROM N.A.
RX STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbavani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celnikier S.,
RA Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AS003820; AAF58429.3; -;
DR EMBL; BT004493; AAO42657.1; -;
DR HSSP; P08581; 1R1W.
DR FlyBase; FBgn0033791; Drl-2.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0004688; F:transferase activity; IEA.
DR GO; GO:0004688; F:transferase activity; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR001245; Tyx_Pkinase.
DR InterPro; IPR008266; Tyx_Pkinase.
DR InterPro; IPR003306; WIF.
DR Pfam; PF02019; WIF; 1.
DR PRINTS; PR0109; TYRKINASE.
DR ProDom; PD000001; Prot kinase; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; UNKNOWN_1.
DR PROSITE; PS50814; WIF; 1.
KW Kinase; Transferase; Tyrosine-protein kinase.
SQ SEQUENCE 648 AA; 71139 MW; 1B4FAA60CB84E457 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 648;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 56 TYAMH 60
|||||

RESULT 12

Q9HGS1 ID Q9HGS1 PRELIMINARY; PRT; 690 AA.
AC Q9HGS1
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Glutaminase (EC 3.5.1.2).
OS Aspergillus oryzae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eutotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5062;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=U212;
RA Thamarongtham C., Turner G., Moir A.J., Tanticharoen M.,
RA Cheevadhanarak S.,
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY005477; AAG02575.1; -;
DR GO; GO:0004359; F:glutaminase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
KW Hydrolase.
SQ SEQUENCE 690 AA; 76226 MW; 6546BE2499D8D43C CRC64;

Query Match 100.0%; Score 29; DB 2; Length 690;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 423 TYAMH 427
|||||

RESULT 13

Q9UVX9 ID Q9UVX9 PRELIMINARY; PRT; 690 AA.
AC Q9UVX9
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Glutaminase A.
GN Name=gtat;

```
OS Aspergillus oryzae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5062;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=RIB40;
RX MEDLINE=20406523; PubMed=10952006;
RT Koibuchi K., Nagasaki H., Yuasa A., Kataoka J., Kitamoto K.;
RT "Molecular cloning and characterization of a gene encoding glutaminase
RT from Aspergillus oryzae.";
RL Appl. Microbiol. Biotechnol. 54:59-68(2000).
DR EMBL; AB029552; BAA86934.1; -.
SQ SEQUENCE 590 AA; 76164 MW; E3D0B17841EEA00D CRC64;

Query Match 100.0%; Score 29; DB 2; Length 590;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
DB 423 TYAMH 427

RESULT 14
V222_FOWPV STANDARD; PRT; 747 AA.
AC Q95Y13;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Putative ankryrin-repeat protein FPV222.
GN Name=FPV222;
OS Fowlpox virus (FPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Avipoxvirus.
OX NCBI_TaxID=10261;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20193820; PubMed=10729156;
RX DOI=10.1128/JVI.74.8.3815-3831.2000;
RT Afonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
RT "The genome of fowlpox virus.";
RL J. Virol. 74:3815-3831(2000).
CC - - SIMILARITY: Contains 14 ANK repeats.
CC -----
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CC -----
CC EMBL; AF198100; AAF44566.1; -.
CC HSSP; Q60778; 10Y3.
CC InterPro; IPR002110; ANK.
CC InterPro; IPR001810; F-box.
CC Pfam; PF00646; F-box; 1.
CC Pfam; PF00646; F-box; 1.
CC PRINTS; PR01415; ANKYRIN.
CC SMART; SM00248; ANK; 15.
CC PROSITE; PS50297; ANK_REPEAT_REGION; 1.
CC PROSITE; PS50086; ANK_REPEAT; 7.
CC ANK repeat; Hypothetical protein; Repeat.
FT REPEAT 38 67 ANK 1.
FT REPEAT 103 132 ANK 2.
FT REPEAT 136 165 ANK 3.
FT REPEAT 169 198 ANK 4.
FT REPEAT 202 231 ANK 5.
FT REPEAT 234 263 ANK 6.
FT REPEAT 294 323 ANK 7.
FT REPEAT 328 357 ANK 8.
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FT REPEAT 361 393 ANK 9.
FT REPEAT 397 426 ANK 10.
FT REPEAT 430 460 ANK 11.
FT REPEAT 464 493 ANK 12.
FT REPEAT 495 524 ANK 13.
FT REPEAT 529 559 ANK 14.
SQ SEQUENCE 747 AA; 85303 MW; 55F90AF2855C3D28 CRC64;

Query Match 100.0%; Score 29; DB 1; Length 747;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
DB 330 TYAMH 334

RESULT 15
Y245_TREPA STANDARD; PRT; 1151 AA.
AC O83273;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Hypothetical protein TP0245.
DE OrderedLocuNames=TP0245;
GN Treponema pallidum.
OS Treponema pallidum.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Nichols;
RX MEDLINE=98332770; PubMed=9665876; DOI=10.1126/science.281.5375.375;
RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA Dodson R.J., Gunn M.L., Hickey E.K., Clayton R.A., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S.L., Peterson J.D.,
RA Khalak H.G., Richardson D.L., Howell J.P., Chidambaram M.,
RA Utterback T.R., McDonald L.A., Artlich P., Bowman C., Cotton M.D.,
RA Fujii C., Garland S.A., Hatch B., Horst K., Roberts K.M., Sandusky M.,
RA Weidman J.F., Smith H.O., Venter J.C.;
RA "Complete genome sequence of Treponema pallidum, the syphilis
RA spirochete.";
RL Science 281:375-388(1998).
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AE001206; AAC65239.1; -.
CC FIR; H71347; H71347.
CC TIGR; TP0245; -.
CC SEQUENCE 1151 AA; 127556 MW; EDB6353C32CB4056 CRC64;

Query Match 100.0%; Score 29; DB 1; Length 1151;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
DB 700 TYAMH 704

Search completed: October 14, 2005, 16:19:49
Job time : 36.2812 secs
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CC cells and platelets. Compositions comprising the antibodies are used for
CC the treatment or prophylaxis of thrombotic or coagulopathic diseases or
CC disorders in a mammal for which inhibiting a FIX/FIXa mediated event is
CC indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable
CC angina, post myocardial infarction, post surgical thrombosis, coronary
CC artery bypass graft (CABG), percutaneous transluminal coronary
CC angioplasty (PTCA), stroke, tumour growth, invasion or metastasis,
CC inflammation, septic shock, hypotension, adult respiratory distress
CC syndrome (ARDS), arterial fibrillation and disseminated intravascular
CC coagulopathy (DIC)
XX
SQ Sequence 17 AA;
Query Match 100.0%; Score 88; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.2e-07; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0;
QY 1 IISYDGSKKYYADSVK 17
Db 1 IISYDGSKKYYADSVK 17
RESULT 2
AB07230
ID ABB07230 standard; protein; 118 AA.
XX
AC ABB07230;
XX
XX
DT 26-MAR-2002 (first entry)
XX
DE Anti-IL-4 receptor MAb 6-2 heavy chain variable region.
XX
XX Human; antibody; interleukin; IL-4; antagonist; receptor; IL-4 receptor;
KW antiarthritic; dermatological; antiulcer; antiinflammatory; cyclostatic;
KW antickling; immunosuppressive; tuberculostatic; ophthalmological;
KW antianemic; antithyroid.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 31..35
FT Region /note= "complementarity determining region (CDR) 1"
FT Region 50..66
FT Region /note= "complementarity determining region (CDR) 2"
FT Region 99..107
FT Region /note= "complementarity determining region (CDR) 3"
XX
XX WO200192340-A2.
XX
XX
XX 06-DEC-2001.
XX
XX 25-MAY-2001; 2001WO-US017094.
XX
XX 26-MAY-2000; 2000US-00579808.
XX 19-SEP-2000; 2000US-00665343.
XX 15-FEB-2001; 2001US-00785934.
XX 01-MAY-2001; 2001US-00847816.
XX
XX (IMMV) IMMUNEX CORP.
XX
XX Pluenneke JD;
XX
XX WPI; 2002-114332/15.
XX N-PSDB; ABA94330.
XX
XX Novel human antibody which binds human interleukin (IL)-4 receptor and is
PT capable of inhibiting IL-4 induced biological activity, functions as IL-4
PT antagonist and is useful for treating septic arthritis, scleroderma.
XX
XX Claim 4; Page 73; 85pp; English.
XX
XX The invention relates to a human antibody (an interleukin (IL)-4
CC antagonist) (I) that binds human IL-4 receptor (IL-4R), and is capable of

CC inhibiting an IL-4-induced biological activity. (I) is also useful for
CC inhibiting both IL-4-induced biological activity and IL-13-induced
CC biological activity in vivo in a human, and for treating septic arthritis
CC in a human afflicted with septic arthritis. (I) is also used for treating
CC conditions such as septic/reactive arthritis, dermatitis herpetiformis,
CC urticaria (especially chronic idiopathic urticaria), ulcers, gastric
CC inflammation, mucosal inflammation, ulcerative colitis, Crohn's disease,
CC inflammatory bowel disease, other disorders of the digestive system in
CC which IL-4 plays a role (e.g. IL-4-induced inflammation of part of the
CC gastrointestinal tract), conditions in which IL-4-induced barrier
CC disruption plays a role (e.g. conditions characterized by decreased
CC epithelial barrier function in the lung or gastrointestinal tract),
CC scleroderma, hypertrophic scarring, Whipple's disease, benign prostate
CC hyperplasia, IL-4-induced pulmonary conditions, allergic reactions to
CC medication, Kawasaki disease, sickle cell disease or crisis, Churg-
CC Straus syndrome, Grave's disease, pre-eclampsia, Sjogren's syndrome,
CC autoimmune lymphoproliferative syndrome, autoimmune haemolytic anemia,
CC Barrett's esophagus, autoimmune uveitis, tuberculosis, nephrosis,
CC pemphigus vulgaris or bullous pemphigoid (autoimmune blistering
CC diseases), and myasthenia gravis (an autoimmune muscular disease). IL-4
CC antagonists also find use as adjuvants to allergy immunotherapy and as
CC vaccine adjuvants, especially when directing the immune response toward a
CC TH1 response would be beneficial in treating or preventing the disease.
CC The present sequence represents an anti-IL-4 receptor monoclonal antibody
CC (MAb) 6-2 heavy chain variable region
XX
XX SQ Sequence 118 AA;
Query Match 98.9%; Score 87; DB 5; Length 118;
Best Local Similarity 94.1%; Pred. No. 4.1e-06; Indels 0; Gaps 0;
Matches 16; Conservative 1; Mismatches 0;
QY 1 IISYDGSKKYYADSVK 17
Db 50 VISYDGSKKYYADSVK 66
RESULT 3
ABP45312
ID ABP45312 standard; protein; 248 AA.
XX
XX AC ABP45312;
XX
XX 19-AUG-2002 (first entry)
XX
XX Human Blys binding scFv SEQ ID 1323.
XX
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
XX Homo sapiens.
XX
XX WO200202641-A1.
XX
XX 10-JAN-2002.
XX
XX 15-JUN-2001; 2001WO-US019110.
XX
XX 16-JUN-2000; 2000US-0212210P.
XX 17-OCT-2000; 2000US-0240816P.
XX 16-MAR-2001; 2001US-0276248P.
XX 21-MAR-2001; 2001US-0277379P.
XX 25-MAY-2001; 2001US-0293499P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX

DR WPI; 2002-114799/15.
XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
XX
PS Claim 1; Page 1981-1982; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 248 AA;

Query Match 98.9%; Score 87; DB 5; Length 248;
Best Local Similarity 94.1%; Pred. No. 9.3e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVK 17
Db 50 VISYDGSKKYYADSVK 66

RESULT 4
ABP44905
ID ABP44905 standard; protein; 248 AA.
XX
AC ABP44905;
XX
XX 19-AUG-2002 (first entry)
XX
XX Human Blys binding scFv SEQ ID 916.
XX
KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
XX WO200202641-A1.
XX
XX 10-JAN-2002.
XX
XX 15-JUN-2001; 2001WO-US019110.
XX
XX 16-JUN-2000; 2000US-0212210P.
XX
XX 17-OCT-2000; 2000US-0240816P.
XX
XX 16-MAR-2001; 2001US-0276248P.
XX
XX 21-MAR-2001; 2001US-0277379P.
XX
XX 25-MAY-2001; 2001US-0293499P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
XX

XX
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
XX diagnosis and treatment of cancers and immune disorders.
XX
XX
PS Claim 1; Page 1495-1496; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 248 AA;

Query Match 98.9%; Score 87; DB 5; Length 248;
Best Local Similarity 94.1%; Pred. No. 9.3e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVK 17
Db 50 VISYDGSKKYYADSVK 66

RESULT 5
ABP44903
ID ABP44903 standard; protein; 248 AA.
XX
AC ABP44903;
XX
XX 19-AUG-2002 (first entry)
XX
XX Human Blys binding scFv SEQ ID 914.
XX
KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
XX WO200202641-A1.
XX
XX 10-JAN-2002.
XX
XX 15-JUN-2001; 2001WO-US019110.
XX
XX 16-JUN-2000; 2000US-0212210P.
XX
XX 17-OCT-2000; 2000US-0240816P.
XX
XX 16-MAR-2001; 2001US-0276248P.
XX
XX 21-MAR-2001; 2001US-0277379P.
XX
XX 25-MAY-2001; 2001US-0293499P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
XX

PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
 PT diagnosis and treatment of cancers and immune disorders.
 XX
 XX
 PS Claim 1; Page 1492-1493; 3148pp; English.
 XX
 CC This invention describes novel antibodies that immunospecifically bind to
 CC B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS
 CC and so may be used to detect and quantitate the presence of BLyS in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of BLyS. They may also be
 CC administered to treat diseases associated with aberrant BLyS expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention
 XX
 XX SQ Sequence 248 AA;
 Query Match 98.9%; Score 87; DB 5; Length 248;
 Best Local Similarity 94.1%; Pred. No. 9.3e-06;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IISYDGSKKYYADSVK 17
 Db 50 VISYDGSKKYYADSVK 66
 RESULT 6
 ADG95730
 ID ADG95730 standard; protein; 248 AA.
 XX
 AC ADG95730;
 XX
 XX 11-MAR-2004 (first entry)
 DT
 DE Single chain antibody that immunospecifically binds BLyS SeqID 914.
 XX
 KW antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor;
 KW B cell proliferation; differentiation; scFv; myasthenia gravis;
 KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
 KW carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
 KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.
 XX
 OS Unidentified.
 XX
 XX WO2003055979-A2.
 PN
 XX 10-JUL-2003.
 PD
 XX 14-NOV-2002; 2002WO-US036496.
 XX
 PF 16-NOV-2001; 2001US-0331469P.
 XX
 PR 19-DEC-2001; 2001US-0340817P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
 PI
 XX WPI; 2003-505530/47.
 DR
 XX Novel antibody that immunospecifically binds to a B lymphocyte stimulator
 PT (BLyS), useful for detecting and treating diseases or disorders e.g.
 PT rheumatoid arthritis, asthma and leukemia.
 XX
 XX Example 1; SEQ ID NO 914; 394pp; English.
 PS
 XX

CC This invention relates to novel antibodies that immunospecifically bind
 CC to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to
 CC chromosome 13q34 and encodes a protein that is a member of the tumour
 CC necrosis factor superfamily and induces both in vivo and in vitro B cell
 CC proliferation and differentiation. Specifically, it refers to single
 CC chain antibody molecules (scFvs) derived, preferably, from the variable
 CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
 CC fragment thereof, of either human, murine, rat or monkey BLyS. The
 CC present invention refers to the use of such antibodies in various methods
 CC for the detection, diagnosis and prognosis of diseases related to the
 CC aberrant expression or inappropriate function of BLyS or its receptor. As
 CC such, these compositions are useful for identifying immune disorders
 CC including myasthenia gravis and multiple sclerosis, inflammatory
 CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
 CC as AIDS and proliferative disorders including leukaemia, carcinoma and
 CC lymphoma. Accordingly, they can be described as exhibiting various
 CC activities such as antirheumatic, antiarthritic, neuroprotective,
 CC antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
 CC polypeptide sequence is a single chain antibody that binds BLyS of the
 CC invention. NOTE: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published pct_sequences.
 XX
 XX SQ Sequence 248 AA;
 Query Match 98.9%; Score 87; DB 7; Length 248;
 Best Local Similarity 94.1%; Pred. No. 9.3e-06;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IISYDGSKKYYADSVK 17
 Db 50 VISYDGSKKYYADSVK 66
 RESULT 7
 ADG95732
 ID ADG95732 standard; protein; 248 AA.
 XX
 AC ADG95732;
 XX
 XX 11-MAR-2004 (first entry)
 DT
 DE Single chain antibody that immunospecifically binds BLyS SeqID 916.
 XX
 KW antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor;
 KW B cell proliferation; differentiation; scFv; myasthenia gravis;
 KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
 KW carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
 KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.
 XX
 OS Unidentified.
 XX
 XX WO2003055979-A2.
 PN
 XX 10-JUL-2003.
 PD
 XX 14-NOV-2002; 2002WO-US036496.
 XX
 PF 16-NOV-2001; 2001US-0331469P.
 XX
 PR 19-DEC-2001; 2001US-0340817P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
 PI
 XX WPI; 2003-505530/47.
 DR
 XX Novel antibody that immunospecifically binds to a B lymphocyte stimulator
 PT (BLyS), useful for detecting and treating diseases or disorders e.g.
 PT rheumatoid arthritis, asthma and leukemia.
 XX
 XX Example 1; SEQ ID NO 916; 394pp; English.
 PS
 XX

CC This invention relates to novel antibodies that immunospecifically bind
 CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
 CC chromosome 13q34 and encodes a protein that is a member of the tumour
 CC necrosis factor superfamily and induces both in vivo and in vitro B cell
 CC proliferation and differentiation. Specifically, it refers to single
 CC chain antibody molecules (scFvs) derived, preferably, from the variable
 CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
 CC fragment thereof, of either human, murine, rat or monkey Blys. The
 CC present invention refers to the use of such antibodies in various methods
 CC for the detection, diagnosis and prognosis of diseases related to the
 CC aberrant expression or inappropriate function of Blys or its receptor. As
 CC such, these compositions are useful for identifying immune disorders
 CC including myasthenia gravis and multiple sclerosis, inflammatory
 CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
 CC as AIDS and proliferative disorders including leukaemia, carcinoma and
 CC lymphoma. Accordingly, they can be described as exhibiting various
 CC activities such as antirheumatic, antiarthritic, neuroprotective,
 CC antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
 CC polypeptide sequence is a single chain antibody that binds Blys of the
 CC invention. NOTE: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published pct_sequences.
 XX
 SQ Sequence 248 AA;

Query Match 98.9%; Score 87; DB 7; Length 248;
 Best Local Similarity 94.1%; Pred. NO. 9.3e-06;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IISYDGSKKYADSVK 17
 :|||||||
 Db 50 VISYDGSKKYADSVK 66

RESULT 8
 ADG96139
 ID ADG96139 standard; protein; 248 AA.
 XX
 AC ADG96139;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Single chain antibody that immunospecifically binds Blys SeqID 1323.
 XX
 KW antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
 KW B cell proliferation; differentiation; scFv; myasthenia gravis;
 KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
 KW carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
 KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.
 XX
 OS Unidentified.

XX
 XX WO2003055979-A2.
 XX
 XX 10-JUL-2003.
 XX
 XX 14-NOV-2002; 2002WO-US036496.
 XX
 XX 16-NOV-2001; 2001US-0331469P.
 XX
 XX 19-DEC-2001; 2001US-0340817P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
 XX
 XX WPI; 2003-505530/47.
 XX
 XX Novel antibody that immunospecifically binds to a B lymphocyte stimulator
 XX (Blys), useful for detecting and treating diseases or disorders e.g.
 XX rheumatoid arthritis, asthma and leukemia.
 XX
 XX Example 1; SEQ ID NO 1323; 394pp; English.

CC This invention relates to novel antibodies that immunospecifically bind
 CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
 CC chromosome 13q34 and encodes a protein that is a member of the tumour
 CC necrosis factor superfamily and induces both in vivo and in vitro B cell
 CC proliferation and differentiation. Specifically, it refers to single
 CC chain antibody molecules (scFvs) derived, preferably, from the variable
 CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
 CC fragment thereof, of either human, murine, rat or monkey Blys. The
 CC present invention refers to the use of such antibodies in various methods
 CC for the detection, diagnosis and prognosis of diseases related to the
 CC aberrant expression or inappropriate function of Blys or its receptor. As
 CC such, these compositions are useful for identifying immune disorders
 CC including myasthenia gravis and multiple sclerosis, inflammatory
 CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
 CC as AIDS and proliferative disorders including leukaemia, carcinoma and
 CC lymphoma. Accordingly, they can be described as exhibiting various
 CC activities such as antirheumatic, antiarthritic, neuroprotective,
 CC antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
 CC polypeptide sequence is a single chain antibody that binds Blys of the
 CC invention. NOTE: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published pct_sequences.
 XX
 SQ Sequence 248 AA;

Query Match 98.9%; Score 87; DB 7; Length 248;
 Best Local Similarity 94.1%; Pred. NO. 9.3e-06;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IISYDGSKKYADSVK 17
 :|||||||
 Db 50 VISYDGSKKYADSVK 66

RESULT 9
 ABP45103
 ID ABP45103 standard; protein; 251 AA.
 XX
 AC ABP45103;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Human Blys binding scFv SEQ ID 1114.
 XX
 KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.

XX
 OS Homo sapiens.
 XX
 XX WO200202641-A1.
 XX
 XX 10-JAN-2002.
 XX
 XX 15-JUN-2001; 2001WO-US019110.
 XX
 XX 16-JUN-2000; 2000US-0212210P.
 XX
 XX 17-OCT-2000; 2000US-0240816P.
 XX
 XX 16-MAR-2001; 2001US-0276248P.
 XX
 XX 21-MAR-2001; 2001US-0277379P.
 XX
 XX 25-MAY-2001; 2001US-0293499P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX
 XX WPI; 2002-114799/15.

PT Antibodies against B lymphocyte stimulating polypeptides, useful for the

XX PS Claim 11; SEQ ID NO 97; 67pp; English.

CC The present invention describes a human heterodimeric antibody (I) (fragment) having a binding affinity of at least 1x10⁻⁸ M to the protective antigen of Bacillus anthracis or a molecule involved in anthrax infection that blocks binding of the antigen or molecule to cell receptors, edema factor and lethal factor. (I) has virucide and antibacterial activities and can be used in immunotherapy. The antibodies (I) are useful as anti-toxins or anti-infectives with respect to infective agents, such as anthrax, botulinum, smallpox, Venezuelan equine encephalomyelitis virus (VERV), or West Nile virus (WNV). The present sequence represents a human heterodimeric antibody heavy chain variable region amino acid sequence, which is used in the exemplification of the present invention.

XX SQ Sequence 135 AA;

Query Match 97.7%; Score 86; DB 7; Length 135;
Best Local Similarity 94.1%; Pred. No. 6.8e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||:|||||

DB 52 IISYDGSKKYYADSVKG 68

RESULT 12

ABB07186

ID ABB07186 standard; protein; 119 AA.

AC ABB07186;

DT 13-MAR-2002 (first entry)

XX SHIGM22 heavy chain variable region clone B sequence.

DE Neuromodulatory; central nervous system; CNS; sHIGM22; LYM 22; AKJR4; ebvHlgM Msl19D10; ebv HlgM CB2bG8; CB2IE12; CB2IE7; MS19E5; virucide; antiparkinsonian; neuroprotective; nootropic; vulnerrary.

XX Homo sapiens.

OS WO200185797-A1.

PN 15-NOV-2001.

PD 30-MAY-2000; 2000WO-US014902.

PF 10-MAY-2000; 2000US-00568351.

PR (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.

PA Rodriguez M, Miller DJ, Pease LR;

PI WPI; 2002-066596/09.

DR N-PSDB; ABA94243.

XX Novel neuromodulatory agent (a human IgM monoclonal antibody), promoting neurite outgrowth, regeneration, remyelination and neuroprotection in central nervous system, useful to treat post-infectious encephalomyelitis.

PT Claim 23; Fig 17; 219pp; English.

XX The invention provides a neuromodulatory agent (I) capable of promoting neurite outgrowth, regeneration, remyelination and neuroprotection in central nervous system (CNS). (I) is capable of inducing remyelination, CC promoting cellular proliferation of glial cells, and promoting Ca²⁺ signaling with oligodendrocytes. An humanised antibody to (I) can be CC selected from antibody sHIGM22 (LYM 22), ebvHlgM Msl19D10, ebv HlgM CC CB2bG8, AKJR4, CB2IE12, CB2IE7 or MS19E5. (I) is useful for stimulating CC remyelination of CNS axons, stimulating proliferation of glial cells in

CC CNS axons, or treating demyelinating disease of CNS in a mammal in need of such therapy. (I) is capable of binding to structures and cells within CNS. (I) is preferably useful for treating a demyelinating disease of CNS of a mouse infected with Strain DA of Theiler's murine encephalomyelitis (TMEV) or for treating a human being having multiple sclerosis, or a human or domestic animal with a viral demyelinating disease, or a post-neural disease of CNS. (I) is also useful for an in vitro method of stimulating the proliferation of glial cells from mixed cell culture. (I) are useful for stimulating remyelination of CNS axons. The antibodies are useful for preventing infection by a bacterium, virus or like pathogen that causes demyelination or other neurodegenerative condition for treating multiple sclerosis, Parkinson's disease, Alzheimer's disease, amyotrophic lateral sclerosis (ALS), a viral demyelinating disease, CNS diseases, and other conditions in the CNS where nerves are damaged as by trauma. The present sequence represents the sHlgM22 heavy chain variable region clone B amino acid sequence

XX SQ Sequence 119 AA;

Query Match 96.6%; Score 85; DB 5; Length 119;
Best Local Similarity 94.1%; Pred. No. 8.6e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||:|||||

DB 50 IISYDGSKKYYADSVKG 66

RESULT 13

ABO33850

ID ABO33850 standard; peptide; 17 AA.

XX ABO33850;

DT 18-SEP-2003 (first entry)

XX Anti-GPI-antibody heavy chain complementarity determining region #10.

DE Human; anti-glucose-6-phosphate isomerase-antibody; immunopolypeptide; anti-GPI-antibody; GPI; glucose-6-phosphate isomerase; autoimmune disease; rheumatoid arthritis; heavy chain variable region; VH; complementarity determining region; CDR.

XX Homo sapiens.

OS US2002146753-A1.

PN 10-OCT-2002.

PD 06-APR-2001; 2001US-00828708.

PF 06-APR-2001; 2001US-00828708.

PR (DITZ/) DITZEL H.

PA (BURT/) BURTON D R.

PA (SCHA/) SCHALLER M.

XX Ditzel H, Burton DR, Schaller M;

PI WPI; 2003-521517/49.

DR Immunopolypeptide for diagnosis and treatment of human autoimmune disease, e.g., human rheumatoid arthritis, comprises a polypeptide that binds to human glucose-6-phosphate isomerase.

XX Claim 3; Fig 4A; 47pp; English.

XX The invention describes an immunopolypeptide comprising a polypeptide that binds to human glucose-6-phosphate isomerase (GPI). The methods and compositions are used for diagnosis and treatment of human autoimmune disease, e.g., human rheumatoid arthritis. This is the amino acid sequence of human anti-GPI-antibody heavy chain variable region

CC complementarity determining region
XX
SQ Sequence 17 AA;

Query Match 95.5%; Score 84; DB 7; Length 112;
Best Local Similarity 88.2%; Pred. No. 1.4e-06;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:||||:|||||
Db 1 VISYDGNKKYYADSVKG 17

RESULT 14
ABO33836
ID ABO33836 standard; protein; 112 AA.
XX
AC ABO33836;
XX
DT 18-SEP-2003 (first entry)
XX
DE Human anti-GPI-antibody heavy chain variable region #3.
XX
KW Human; anti-glucose-6-phosphate isomerase-antibody; immunopolypeptide;
KW anti-GPI-antibody; GPI; glucose-6-phosphate isomerase;
KW autoimmune disease; rheumatoid arthritis; heavy chain variable region;
KW VH.
XX
OS Homo sapiens.
XX
PN US2002146753-A1.
XX
PD 10-OCT-2002.
XX
PF 06-APR-2001; 2001US-00828708.
XX
PR 06-APR-2001; 2001US-00828708.
XX
PA (DITZ/) DITZEL H.
PA (BURT/) BURTON D R.
PA (SCHA/) SCHALLER M.
XX
PI Ditzel H, Burton DR, Schaller M;
XX WPI; 2003-521517/49.
XX
DR Immunopolypeptide for diagnosis and treatment of human autoimmune
PT disease, e.g., human rheumatoid arthritis, comprises a polypeptide that
PT binds to human glucose-6-phosphate isomerase.
XX
PS Claim 11; Fig 3AH; 47pp; English.
XX
CC The invention describes an immunopolypeptide comprising a polypeptide
CC that binds to human glucose-6-phosphate isomerase (GPI). The methods and
CC compositions are used for diagnosis and treatment of human autoimmune
CC disease, e.g., human rheumatoid arthritis. This is the amino acid
CC sequence of human anti-GPI-antibody heavy chain variable region
XX
SQ Sequence 112 AA;

Query Match 95.5%; Score 84; DB 7; Length 112;
Best Local Similarity 88.2%; Pred. No. 1.2e-05;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:||||:|||||
Db 43 VISYDGNKKYYADSVKG 59

RESULT 15
ABB07169
ID ABB07169 standard; protein; 119 AA.
XX

AC ABB07169;
XX
DT 13-MAR-2002 (first entry)
XX
DE sHlgM22 heavy chain variable region clone A sequence.
XX
KW Neuromodulatory; central nervous system; CNS; sHlgM22; LYM 22; AKJR4;
KW ebvHlgM M8119D10; ebv HlgM CB2BG8; CB2IE12; CB2IE7; MS119E5; virucide;
KW antiparkinsonian; neuroprotective; nootropic; vulnery.
XX
OS Homo sapiens.
XX
PN WO200185797-A1.
XX
PD 15-NOV-2001.
XX
PF 30-MAY-2000; 2000WO-US014902.
XX
PR 10-MAY-2000; 2000US-00568351.
XX
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.
XX
PI Rodriguez M, Miller DJ, Pease LR;
XX WPI; 2002-066596/09.
XX N-PSDB; ABA94216.
XX
PT Novel neuromodulatory agent (a human IgM monoclonal antibody), promoting
PT neurite outgrowth, regeneration, remyelination and neuroprotection in
PT central nervous system, useful to treat post-infectious
PT encephalomyelitis.
XX
PS Claim 23; Fig 17; 219pp; English.
XX
CC The invention provides a neuromodulatory agent (I) capable of promoting
CC neurite outgrowth, regeneration, remyelination and neuroprotection in
CC central nervous system (CNS). (I) is capable of inducing remyelination,
CC promoting cellular proliferation of glial cells, and promoting Ca²⁺
CC signaling with oligodendrocytes. An humanised antibody to (I) can be
CC selected from antibody sHlgM22 (LYM 22), ebvHlgM M8119D10, ebv HlgM
CC CB2BG8, AKJR4, CB2IE12, CB2IE7 or MS119E5. (I) is useful for stimulating
CC remyelination of CNS axons, stimulating proliferation of glial cells in
CC CNS axons, or treating demyelinating disease of CNS in a mammal in need
CC of such therapy. (I) is capable of binding to structures and cells within
CC CNS. (I) is preferably useful for treating a demyelinating disease of CNS
CC of a mouse infected with Strain DA of Theiler's murine encephalomyelitis
CC (TMEM) or for treating a human being having multiple sclerosis, or a
CC human or domestic animal with a viral demyelinating disease, or a post-
CC neural disease of CNS. (I) is also useful for an in vitro method of
CC stimulating the proliferation of glial cells from mixed cell culture. (I)
CC is also useful for stimulating remyelination of CNS axons. The antibodies
CC are useful for preventing infection by a bacterium, virus or like
CC pathogen that causes demyelination or other neurodegenerative condition
CC in a subject. Methods where (I) is administered to a patient are useful
CC for treating multiple sclerosis, Parkinson's disease, Alzheimer's
CC disease, amyotrophic lateral sclerosis (ALS), a viral demyelinating
CC disease, CNS diseases, and other conditions in the CNS where nerves are
CC damaged as by trauma. The present sequence represents the sHlgM22 heavy
CC chain variable region clone A amino acid sequence
XX
SQ Sequence 119 AA;

Query Match 95.5%; Score 84; DB 5; Length 119;
Best Local Similarity 88.2%; Pred. No. 1.3e-05;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:||||:|||||
Db 50 VISYDGNKKYYADSVKG 66

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Job time : 132.688 secs

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OM protein - protein search, using sw model

Run on: October 14, 2005, 16:00:04 ; Search time 33.4688 Seconds
(without alignments)
37.917 Million cell updates/sec

Title: US-10-614-959-11
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Sequence: 1 IISYDGSKKYADSVKG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/ptodata/1/iaa/PTUS-COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	88	100.0	17	4	US-09-383-667-11	Sequence 11, Appl
2	83	94.3	17	4	US-09-383-667-18	Sequence 18, Appl
3	82	93.2	17	4	US-09-383-667-16	Sequence 16, Appl
4	82	93.2	17	4	US-09-383-667-20	Sequence 20, Appl
5	82	93.2	17	4	US-09-424-840B-36	Sequence 36, Appl
6	82	93.2	17	4	US-09-424-840B-95	Sequence 95, Appl
7	82	93.2	17	4	US-09-424-840B-97	Sequence 97, Appl
8	82	93.2	17	4	US-09-424-840B-108	Sequence 108, Appl
9	82	93.2	98	1	US-08-211-202-118	Sequence 118, Appl
10	82	93.2	115	4	US-09-726-219A-167	Sequence 167, Appl
11	82	93.2	116	1	US-08-211-202-141	Sequence 141, Appl
12	82	93.2	117	3	US-08-545-809A-115	Sequence 115, App
13	82	93.2	119	2	US-08-331-398A-46	Sequence 46, Appl
14	82	93.2	119	2	US-08-331-397B-46	Sequence 46, Appl
15	82	93.2	119	2	US-08-759-804A-46	Sequence 46, Appl
16	82	93.2	119	3	US-09-227-693-46	Sequence 46, Appl
17	82	93.2	120	1	US-08-211-202-135	Sequence 135, Appl
18	82	93.2	120	1	US-07-942-245-35	Sequence 35, Appl
19	82	93.2	123	3	US-08-983-607-38	Sequence 38, Appl
20	82	93.2	123	4	US-09-424-840B-6	Sequence 6, Appl
21	82	93.2	128	1	US-08-478-039-96	Sequence 96, Appl
22	82	93.2	128	1	US-08-476-349A-96	Sequence 96, Appl
23	82	93.2	248	4	US-03-315-926A-80	Sequence 80, Appl
24	81	92.0	17	4	US-09-424-840B-77	Sequence 77, Appl
25	81	92.0	17	4	US-09-424-840B-111	Sequence 111, App
26	81	92.0	124	4	US-09-424-840B-16	Sequence 16, Appl
27	81	92.0	179	3	US-08-862-124-2	Sequence 2, Appli

28	81	92.0	225	4	US-09-456-090A-102	Sequence 102, App
29	81	92.0	225	4	US-09-456-090A-108	Sequence 108, App
30	81	92.0	225	4	US-09-456-090A-110	Sequence 110, App
31	81	92.0	225	4	US-09-453-234-102	Sequence 102, App
32	81	92.0	225	4	US-09-453-234-108	Sequence 108, App
33	81	92.0	225	4	US-09-453-234-110	Sequence 110, App
34	81	92.0	287	3	US-08-862-124-17	Sequence 17, Appl
35	81	92.0	304	3	US-08-862-124-14	Sequence 14, Appl
36	79	89.8	17	4	US-09-560-198A-12	Sequence 12, Appl
37	79	89.8	17	4	US-09-424-840B-84	Sequence 84, Appl
38	79	89.8	17	4	US-09-424-840B-113	Sequence 113, App
39	79	89.8	123	4	US-09-560-198A-2	Sequence 2, Appl1
40	79	89.8	123	4	US-09-560-198A-4	Sequence 4, Appl1
41	79	89.8	123	4	US-09-560-198A-10	Sequence 10, Appl
42	79	89.8	123	4	US-09-424-840B-22	Sequence 22, Appl
43	77	87.5	126	1	US-08-276-852-81	Sequence 81, Appl
44	77	87.5	126	1	US-08-899-575-81	Sequence 81, Appl
45	77	87.5	126	1	US-08-899-575-81	Sequence 81, Appl

ALIGNMENTS

RESULT 1
US-09-383-667-11
; Sequence 11, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camelia W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Eaton, Dan L.
; APPLICANT: Hass, Phillip E.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Kirchofer, Daniel
; APPLICANT: Suggett, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: P1661R2
; CURRENT APPLICATION NUMBER: US/09/383,667
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,233
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: US 60/122,767
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 11
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-667-11
Query Match 100.0%; Score 88; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 IISYDGSKKYADSVKG 17
Db 1 IISYDGSKKYADSVKG 17
RESULT 2
US-09-383-667-18
; Sequence 18, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camelia W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Eaton, Dan L.
; APPLICANT: Hass, Phillip E.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Kirchofer, Daniel
; APPLICANT: Suggett, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: P1661R2

; CURRENT APPLICATION NUMBER: US/09/383,667
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,233
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: US 60/122,767
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-667-18

Query Match 94.3%; Score 83; DB 4; Length 17;
Best Local Similarity 94.1%; Pred. No. 8.1e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
| | | | | | | | | | | | | | | | | |
Db 1 IISYDGSNKYYADSVKG 17

RESULT 3
US-09-383-667-16
; Sequence 16, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camelia W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Eaton, Dan L.
; APPLICANT: Hass, Philip E.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Kirchhofer, Daniel
; APPLICANT: Suggestt, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: P1661R2
; CURRENT APPLICATION NUMBER: US/09/383,667
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,233
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: US 60/122,767
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 16
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-667-16

Query Match 93.2%; Score 82; DB 4; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
| | | | | | | | | | | | | | | | | |
Db 1 VISYDGSNKYYADSVKG 17

RESULT 4
US-09-383-667-20
; Sequence 20, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camelia W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Eaton, Dan L.
; APPLICANT: Hass, Philip E.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Kirchhofer, Daniel
; APPLICANT: Suggestt, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: P1661R2
; CURRENT APPLICATION NUMBER: US/09/383,667

; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,233
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: US 60/122,767
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 20
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-667-20

Query Match 93.2%; Score 82; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVK 16
| | | | | | | | | | | | | | | | | |
Db 1 IISYDGSKKYYADSVK 16

RESULT 5
US-09-424-840B-36
; Sequence 36, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424,840B
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-424-840B-36

Query Match 93.2%; Score 82; DB 4; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
| | | | | | | | | | | | | | | | | |
Db 1 VISYDGSNKYYADSVKG 17

RESULT 6
US-09-424-840B-95
; Sequence 95, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424,840B
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128

SOFTWARE: PatentIn version 3.1
SEQ ID NO 95
LENGTH: 17
TYPE: PRT
ORGANISM: Homo sapiens
US-09-424-840B-95

Query Match 93.2%; Score 82; DB 4; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYADSVKG 17
:|||||
Db 1 VISYDGSNKYADSVKG 17

RESULT 7

US-09-424-840B-97
Sequence 97, Application US/09424840B
Patent No. 6790938
GENERAL INFORMATION:
APPLICANT: Berchtold, Peter
TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
FILE REFERENCE: 100564-09049
CURRENT APPLICATION NUMBER: US/09/424,840B
CURRENT FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: DE 19820663.1
PRIOR FILING DATE: 1998-05-08
PRIOR APPLICATION NUMBER: DE 19755227.7
PRIOR FILING DATE: 1997-12-12
PRIOR APPLICATION NUMBER: DE 19723904.8
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PatentIn version 3.1
SEQ ID NO 97
LENGTH: 17
TYPE: PRT
ORGANISM: Homo sapiens
US-09-424-840B-97

Query Match 93.2%; Score 82; DB 4; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYADSVKG 17
:|||||
Db 1 VISYDGSNKYADSVKG 17

RESULT 8

US-09-424-840B-108
Sequence 108, Application US/09424840B
Patent No. 6790938
GENERAL INFORMATION:
APPLICANT: Berchtold, Peter
TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
FILE REFERENCE: 100564-09049
CURRENT APPLICATION NUMBER: US/09/424,840B
CURRENT FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: DE 19820663.1
PRIOR FILING DATE: 1998-05-08
PRIOR APPLICATION NUMBER: DE 19755227.7
PRIOR FILING DATE: 1997-12-12
PRIOR APPLICATION NUMBER: DE 19723904.8
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PatentIn version 3.1
SEQ ID NO 108
LENGTH: 17
TYPE: PRT
ORGANISM: Homo sapiens

US-09-424-840B-108

Query Match 93.2%; Score 82; DB 4; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYADSVKG 17
:|||||
Db 1 VISYDGSNKYADSVKG 17

RESULT 9

US-08-211-202-118
Sequence 118, Application US/08211202
Patent No. 5565332
GENERAL INFORMATION:
APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matteus
APPLICANT: BAIER, Michael
APPLICANT: JESPERS, Laurent Stephane Anne Therese
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: Production of chimeric antibodies - a
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,202
FILING DATE: 23-SEP-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120252.3
FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120377.8
FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/31960
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 118:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-211-202-118

Query Match 93.2%; Score 82; DB 1; Length 98;
Best Local Similarity 88.2%; Pred. No. 7.3e-06;

Matches 15; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:||||| |||||||
Db 50 VISYDGSNKKYYADSVKG 66

RESULT 10
US-09-726-219A-167
; Sequence 167, Application US/09726219A
; Patent No. 6806079
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clarkson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 213839-00013
; CURRENT APPLICATION NUMBER: US/09/726,219A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 167
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-726-219A-167

Query Match 93.2%; Score 82; DB 4; Length 115;
Best Local Similarity 88.2%; Pred. No. 8.6e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:||||| |||||||
Db 50 VISYDGSNKKYYADSVKG 66

RESULT 11
US-08-211-202-141
; Sequence 141, Application US/08211202
; Patent No. 5565332
; GENERAL INFORMATION:
; APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Mattheus
; APPLICANT: BAIER, Michael

APPLICANT: JESPERS, Laurent Stephane Anne Therese
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: Production of chimeric antibodies - a
TITLE OF INVENTION: combinatorial approach
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,202
FILING DATE: 23-SEP-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120252.3
FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120377.8
FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/31960
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 141:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-211-202-141

Query Match 93.2%; Score 82; DB 1; Length 116;
Best Local Similarity 88.2%; Pred. No. 8.7e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:||||| |||||||
Db 50 VISYDGSNKKYYADSVKG 66

RESULT 12
US-08-545-809A-115
; Sequence 115, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:


```
; ADDRESS: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-545-809A-115

Query Match 93.2%; Score 82; DB 3; Length 117;
Best Local Similarity 88.2%; Pred. No. 8.8e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
Db 69 VISYDGSNKYYADSVKG 85

RESULT 13
US-08-331-398A-46
; Sequence 46, Application US/08331398A
; Patent No. 5608039
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: FitzGerald, David
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
; TITLE OF INVENTION: and Their Uses (as amended)
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; STREET: Townsend and Townsend and Crew
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331.398A
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331

Query Match 93.2%; Score 82; DB 1; Length 119;
Best Local Similarity 88.2%; Pred. No. 8.9e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
Db 50 VISYDGSNKYYADSVKG 66

RESULT 14
US-08-331-397B-46
; Sequence 46, Application US/08331397B
; Patent No. 5981726
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Benhar, Itai
; TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
; TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; STREET: Townsend and Townsend and Crew
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331.397B
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126120US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
```

TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION: /note= "Human fetal immunoglobulin
OTHER INFORMATION: 56PI'CL Variable Heavy chain (V-H)"
US-08-331-397B-46
Query Match 93.2%; Score 82; DB 2; Length 119;
Best Local Similarity 88.2%; Pred. No. 8.9e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 IISYDGSKKYYADSVKG 17
Db 50 VISYDGSNKYYADSVKG 66
RESULT 15
US-08-759-804A-46
Sequence 46, Application US/08759804A
Patent No. 5990296
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Willingham, Mark
APPLICANT: FitzGerald, David J.
APPLICANT: Brinkmann, Ulrich
APPLICANT: Pai, Lee
TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,804A
FILING DATE: 03-DEC-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/331,398
FILING DATE: 28-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 015280-126140US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid

STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION: /note= "Human fetal immunoglobulin
OTHER INFORMATION: 56PI'CL Variable Heavy chain (V-H)"
US-08-759-804A-46
Query Match 93.2%; Score 82; DB 2; Length 119;
Best Local Similarity 88.2%; Pred. No. 8.9e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 IISYDGSKKYYADSVKG 17
Db 50 VISYDGSNKYYADSVKG 66
Search completed: October 14, 2005, 16:22:00
Job time : 33.4688 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2005, 16:20:10 ; Search time 120.859 Seconds
(without alignments)
58.615 Million cell updates/sec

Title: US-10-614-959-11

Perfect score: 88

Sequence: 1 IISYDGSKKYADSVKVG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1859788 seqs, 416717961 residues

Total number of hits satisfying chosen parameters: 1859788

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0*

Maximum Match 100*

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Database :

- Published Applications AA:*
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 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
 - 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
 - 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
 - 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
 - 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
 - 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
 - 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	87	98.9	17	US-10-989-462-300	Sequence 300, App
2	87	98.9	121	US-10-989-462-262	Sequence 262, App
3	87	98.9	248	US-09-880-748-914	Sequence 914, App
4	87	98.9	248	US-09-880-748-916	Sequence 916, App
5	87	98.9	248	US-09-880-748-1323	Sequence 1323, App
6	87	98.9	248	US-10-293-418-914	Sequence 914, App
7	87	98.9	248	US-10-293-418-916	Sequence 916, App
8	87	98.9	248	US-10-293-418-1323	Sequence 1323, App
9	87	98.9	251	US-09-880-748-1114	Sequence 1114, App
10	87	98.9	251	US-10-293-418-1114	Sequence 1114, App
11	87	98.9	252	US-10-989-462-276	Sequence 276, App

12	86	97.7	135	15	US-10-364-743-97	Sequence 97, Appl
13	86	97.7	135	16	US-10-452-593-97	Sequence 97, Appl
14	84	95.5	17	9	US-09-828-708-24	Sequence 24, Appl
15	84	95.5	17	17	US-10-630-009-24	Sequence 24, Appl
16	84	95.5	101	9	US-09-828-708-10	Sequence 10, Appl
17	84	95.5	101	17	US-10-630-009-10	Sequence 10, Appl
18	84	95.5	119	14	US-10-010-729-7	Sequence 7, Appl
19	83	94.3	123	17	US-10-727-155-14	Sequence 14, Appl
20	83	94.3	125	15	US-10-292-088-58	Sequence 58, Appl
21	83	94.3	137	15	US-10-364-743-11	Sequence 11, Appl
22	83	94.3	137	15	US-10-364-743-99	Sequence 99, Appl
23	83	94.3	137	16	US-10-452-593-11	Sequence 11, Appl
24	83	94.3	137	16	US-10-452-593-99	Sequence 99, Appl
25	83	94.3	252	10	US-09-880-748-1690	Sequence 1690, Ap
26	83	94.3	252	15	US-10-293-418-1690	Sequence 1690, Ap
27	83	94.3	470	15	US-10-292-088-62	Sequence 62, Appl
28	82	93.2	17	10	US-09-972-656-48	Sequence 48, Appl
29	82	93.2	17	15	US-10-384-060-46	Sequence 46, Appl
30	82	93.2	17	15	US-10-399-701-6	Sequence 6, Appl
31	82	93.2	17	16	US-10-396-578-21	Sequence 21, Appl
32	82	93.2	17	16	US-10-396-578-39	Sequence 39, Appl
33	82	93.2	17	16	US-10-396-578-51	Sequence 51, Appl
34	82	93.2	17	16	US-10-396-578-81	Sequence 81, Appl
35	82	93.2	17	16	US-10-844-424-36	Sequence 36, Appl
36	82	93.2	17	16	US-10-844-424-95	Sequence 95, Appl
37	82	93.2	17	16	US-10-844-424-97	Sequence 97, Appl
38	82	93.2	17	16	US-10-844-424-108	Sequence 108, App
39	82	93.2	17	16	US-10-798-380-23	Sequence 23, Appl
40	82	93.2	17	17	US-10-726-332-114	Sequence 114, App
41	82	93.2	17	20	US-11-074-803-21	Sequence 21, Appl
42	82	93.2	17	20	US-11-074-803-39	Sequence 39, Appl
43	82	93.2	17	20	US-11-074-803-51	Sequence 51, Appl
44	82	93.2	17	20	US-11-074-803-81	Sequence 81, Appl
45	82	93.2	41	15	US-10-269-711-47	Sequence 47, Appl

ALIGNMENTS

RESULT 1
US-10-989-462-300
; Sequence 300, Application US/10989462
; Publication No. US20050220795A1
; GENERAL INFORMATION:
; APPLICANT: Witttrup, K. Dane
; APPLICANT: Yeung, Yik Andy
; TITLE OF INVENTION: ANTI-HYDROXYLASE ANTIBODIES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 01997-325001
; CURRENT APPLICATION NUMBER: US/10/989,462
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/520,114
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US 60/563,514
; PRIOR FILING DATE: 2004-04-19
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 300
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-989-462-300

Query Match 98.9%; Score 87; DB 18; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.6e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYADSVKVG 17

Db 1 VISYDGSKKYADSVKVG 17

RESULT 4
 US-09-880-748-916
 ; Sequence 916, Application US/09880748
 ; Publication No. US20030059937A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; FILE REFERENCE: PF523
 ; CURRENT APPLICATION NUMBER: US/09/880,748
 ; CURRENT FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/212,210
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; NUMBER OF SEQ ID NOS: 3239
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 916
 ; LENGTH: 248
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-880-748-916

Query Match 98.9%; Score 87; DB 10; Length 248;
 Best Local Similarity 94.1%; Pred. No. 2.5e-05;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
 :|||||
 Db 50 VISYDGSKKYYADSVKG 66

RESULT 5
 US-09-880-748-1323
 ; Sequence 1323, Application US/09880748
 ; Publication No. US20030059937A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; FILE REFERENCE: PF523
 ; CURRENT APPLICATION NUMBER: US/09/880,748
 ; CURRENT FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/212,210
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; NUMBER OF SEQ ID NOS: 3239
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 1323
 ; LENGTH: 248
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-880-748-1323

Query Match 98.9%; Score 87; DB 10; Length 248;
 Best Local Similarity 94.1%; Pred. No. 2.5e-05;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
 :|||||
 Db 50 VISYDGSKKYYADSVKG 66

RESULT 2
 US-10-989-462-262
 ; Sequence 262, Application US/10989462
 ; Publication No. US20050220795A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wittrup, K. Dane
 ; APPLICANT: Yeung, Yik Andy
 ; TITLE OF INVENTION: ANTI-HYDROXYLASE ANTIBODIES AND USES
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: 01997-329001
 ; CURRENT APPLICATION NUMBER: US/10/989,462
 ; CURRENT FILING DATE: 2004-11-15
 ; PRIOR APPLICATION NUMBER: US 60/520,114
 ; PRIOR FILING DATE: 2003-11-14
 ; PRIOR APPLICATION NUMBER: US 60/563,514
 ; PRIOR FILING DATE: 2004-04-19
 ; NUMBER OF SEQ ID NOS: 319
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 262
 ; LENGTH: 121
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetically generated peptide
 US-10-989-462-262

Query Match 98.9%; Score 87; DB 18; Length 121;
 Best Local Similarity 94.1%; Pred. No. 1.2e-05;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
 :|||||
 Db 50 VISYDGSKKYYADSVKG 66

RESULT 3
 US-09-880-748-914
 ; Sequence 914, Application US/09880748
 ; Publication No. US20030059937A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; FILE REFERENCE: PF523
 ; CURRENT APPLICATION NUMBER: US/09/880,748
 ; CURRENT FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/212,210
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; NUMBER OF SEQ ID NOS: 3239
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 914
 ; LENGTH: 248
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-880-748-914

Query Match 98.9%; Score 87; DB 10; Length 248;
 Best Local Similarity 94.1%; Pred. No. 2.5e-05;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
 :|||||
 Db 50 VISYDGSKKYYADSVKG 66

RESULT 6
US-10-293-418-914
; Sequence 914, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 914
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-914

Query Match 98.9%; Score 87; DB 15; Length 248;
Best Local Similarity 94.1%; Pred. No. 2.5e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 IISYDGSKKYYADSVKG 17
Db 50 VISYDGSKKYYADSVKG 66

RESULT 7
US-10-293-418-916
; Sequence 916, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 916
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens

; ORGANISM: Homo sapiens
US-10-293-418-916
Query Match 98.9%; Score 87; DB 15; Length 248;
Best Local Similarity 94.1%; Pred. No. 2.5e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 IISYDGSKKYYADSVKG 17
Db 50 VISYDGSKKYYADSVKG 66

RESULT 8
US-10-293-418-1323
; Sequence 1323, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1323
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1323

Query Match 98.9%; Score 87; DB 15; Length 248;
Best Local Similarity 94.1%; Pred. No. 2.5e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 IISYDGSKKYYADSVKG 17
Db 50 VISYDGSKKYYADSVKG 66

RESULT 9
US-09-880-748-1114
; Sequence 1114, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499

Query Match	Best Local Similarity	Score	DB	Length	Indels	Mismatches	Gaps
Query Match	Best Local Similarity	98.9%	Score 87;	DB 10;	Length 251;		
Matches 16;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;			
QY	1 IISYDGSKKYYADSVKG 17						
Db	50 VISYDGSKKYYADSVKG 66						
RESULT 10	US-10-293-418-1114						
Sequence 1114,	Application US/10293418						
Publication No.	US20030223996A1						
GENERAL INFORMATION:							
APPLICANT:	Ruben et al.						
TITLE OF INVENTION:	Antibodies that Immunospecifically Bind Blys						
FILE REFERENCE:	PF23P2						
CURRENT APPLICATION NUMBER:	US/10/293,418						
CURRENT FILING DATE:	2002-11-27						
PRIOR APPLICATION NUMBER:	60/331,469						
PRIOR FILING DATE:	2001-11-16						
PRIOR APPLICATION NUMBER:	60/340,817						
PRIOR FILING DATE:	2001-12-19						
PRIOR APPLICATION NUMBER:	09/880,748						
PRIOR FILING DATE:	2001-06-15						
PRIOR APPLICATION NUMBER:	60/293,499						
PRIOR FILING DATE:	2001-05-25						
PRIOR APPLICATION NUMBER:	60/277,379						
PRIOR FILING DATE:	2001-03-21						
PRIOR APPLICATION NUMBER:	60/276,248						
PRIOR FILING DATE:	2001-03-16						
PRIOR APPLICATION NUMBER:	60/240,816						
PRIOR FILING DATE:	2000-10-17						
PRIOR APPLICATION NUMBER:	60/212,210						
PRIOR FILING DATE:	2000-06-16						
NUMBER OF SEQ ID NOS:	3247						
SEQ ID NO 1114							
LENGTH: 251							
TYPE: PRT							
ORGANISM: Homo sapiens							
US-10-293-418-1114							
Query Match	Best Local Similarity	98.9%	Score 87;	DB 15;	Length 251;		
Matches 16;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;			
QY	1 IISYDGSKKYYADSVKG 17						
Db	50 VISYDGSKKYYADSVKG 66						
RESULT 11	US-10-989-462-276						
Sequence 276,	Application US/10989462						
Publication No.	US20050220795A1						
GENERAL INFORMATION:							
APPLICANT:	Wittup, K. Dane						
TITLE OF INVENTION:	ANTI-HYDROXYLASE ANTIBODIES AND USES						
FILE REFERENCE:	01997-329001						
CURRENT APPLICATION NUMBER:	US/10/989,462						
PRIOR FILING DATE:	2004-11-15						
PRIOR APPLICATION NUMBER:	US 60/520 114						

PRIOR APPLICATION NUMBER: US 60/376,408
PRIOR FILING DATE: 2002-04-29
PRIOR APPLICATION NUMBER: US 60/428,807
PRIOR FILING DATE: 2002-11-25
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.2
SEQ ID NO 97
LENGTH: 135
TYPE: PRT
ORGANISM: human
US-10-452-593-97

Query Match
Best Local Similarity 97.7%; Score 86; DB 16; Length 135;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
Db 52 LISYDGSKKYYADSVKG 68

RESULT 14
US-09-828-708-24
Sequence 24, Application US/09828708
Patent No. US20020146753A1
GENERAL INFORMATION:
APPLICANT: Burton, D.
APPLICANT: Schaller, M.
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
FILE REFERENCE: 1361.005US1
CURRENT APPLICATION NUMBER: US/09/828,708
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 24
LENGTH: 17
TYPE: PRT
ORGANISM: Homo sapiens
US-09-828-708-24

Query Match
Best Local Similarity 95.5%; Score 84; DB 9; Length 17;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
Db 1 VISYDGNKKYYADSVKG 17

RESULT 15
US-10-630-009-24
Sequence 24, Application US/10630009
Publication No. US2005080239A1
GENERAL INFORMATION:
APPLICANT: Burton, D.
APPLICANT: Schaller, M.
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
FILE REFERENCE: 1361.005US2
CURRENT APPLICATION NUMBER: US/10/630,009
CURRENT FILING DATE: 2003-07-29
PRIOR APPLICATION NUMBER: US 09/828,708
PRIOR FILING DATE: 2001-04-06
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 24
LENGTH: 17
TYPE: PRT
ORGANISM: Homo sapiens
US-10-630-009-24

Query Match
Best Local Similarity 95.5%; Score 84; DB 17; Length 17;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
Db 1 VISYDGNKKYYADSVKG 17

Search completed: October 14, 2005, 17:00:42
Job time : 121.859 secs

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OM protein - protein search, using sw model

Run on: October 14, 2005, 16:02:59 ; Search time 23.6406 Seconds
(without alignments)
69.190 Million cell updates/sec

Title: US-10-614-959-11
Perfect score: 88
Sequence: 1 IISYDGSKKYADSVKG 17

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Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	82	93.2	94	2	PL0120
2	82	93.2	97	2	S44115
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5	82	93.2	109	2	PH1645
6	82	93.2	109	2	PH1644
7	82	93.2	111	2	PH1643
8	82	93.2	111	2	PH1645
9	82	93.2	113	2	S38490
10	82	93.2	114	2	S46390
11	82	93.2	114	2	S46392
12	82	93.2	117	2	S36270
13	82	93.2	118	2	S31677
14	82	93.2	118	2	S31116
15	82	93.2	119	2	S36005
16	82	93.2	120	2	S31112
17	82	93.2	121	2	S19666
18	82	93.2	121	2	S36005
19	82	93.2	122	2	S36005
20	82	93.2	122	2	S31119
21	82	93.2	123	2	S38493
22	82	93.2	130	2	PL0098
23	82	93.2	132	2	S31603
24	82	93.2	134	2	S31679
25	82	93.2	139	2	S31674
26	77	87.5	137	2	S31701
27	75	85.2	108	2	PH1642
28	75	85.2	114	2	S46391
29	75	85.2	119	2	S31111

30	75	85.2	122	2	S31117	Ig heavy chain - h
31	75	85.2	128	2	S48797	Ig heavy chain v r
32	75	85.2	133	2	A49028	Ig heavy chain v-i
33	75	85.2	133	2	S31510	Ig heavy chain - h
34	74	84.1	98	2	S28543	Ig heavy chain v r
35	74	84.1	117	2	S38259	Ig heavy chain v r
36	74	84.1	118	2	PH1662	Ig heavy chain v r
37	74	84.1	122	1	M3HUAM	Ig heavy chain v-i
38	74	84.1	134	2	S31688	Ig heavy chain v r
39	74	84.1	135	2	S31598	Ig heavy chain v r
40	74	84.1	140	2	S70442	Ig heavy chain v r
41	73	83.0	151	2	A60943	Ig heavy chain pre
42	72	81.8	115	2	S38284	Ig heavy chain v r
43	72	81.8	121	2	PH1661	Ig heavy chain v r
44	71	80.7	118	2	PH1660	Ig heavy chain v r
45	69	78.4	76	2	S31592	Ig heavy chain v r

ALIGNMENTS

RESULT 1
PL0120
Ig heavy chain V-III region (TD-Vo) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C:Accession: PL0120
R:Bird, J.; Galili, N.; Link, M.; Stites, D.; Sklar, J.
J. Exp. Med. 168, 229-245, 1988
A:Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin
A:Reference number: PL0116; MUID:88286083; PMID:2840480
A:Accession: PL0120
A:Molecule type: mRNA
A:Residues: 1-94 <BIR>
A:Cross-references: UNIPROT:Q8WUK1; UNIPROT:Q9UL93
A:Experimental source: B cells from patient TD with acute lymphoblastic leukemia, ALL
A>Note: the sequence shows the V region (TD-Vo) from a nonproductive DNA rearrangement f
C:Superfamily: immunoglobulin v region; immunoglobulin homology
C:Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin
F:31-35/Region: complementarity-determining 1
F:49-65/Region: complementarity-determining 2
Query Match 93.2%; Score 82; DB 2; Length 94;
Best Local Similarity 88.2%; Pred. No. 7.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 IISYDGSKKYADSVKG 17
Db 50 VISYDGSNKYADSVKG 66
RESULT 2
S44115
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C:Accession: S44115
R:Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A:Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable re
A:Reference number: S44105
A:Accession: S44115
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-97 <HAW>
A:Cross-references: EMBL:Z31384; NID:9472969; PIDN:CAA83259.1; PID:940526
C:Superfamily: immunoglobulin v region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
Query Match 93.2%; Score 82; DB 2; Length 97;
Best Local Similarity 88.2%; Pred. No. 7.5e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKVG 17
:|||||
Db 50 VISYDGSNKYYADSVKVG 66

RESULT 3
PL0116
Ig heavy chain V-III region (AW-Vx) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Jul-1999
C;Accession: PL0116; S26892
R;Bird, J.; Galili, N.; Link, M.; Stites, D.; Sklar, J.
J. Exp. Med. 168, 225-245, 1988
A;Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin
A;Reference number: PL0116; MUID:88286089; PMID:2840480
A;Accession: PL0116
A;Molecule type: mRNA
A;Residues: 1-98 <BIR>
A;Experimental source: B cells from patient AW with acute lymphoblastic leukemia, ALL
A;Note: the sequence shows the V region (AW-Vx) from a nonproductive DNA rearrangement
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26892
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: EMBL:Z12349; NID:g32918; PIDN:CAA78219.1; PID:g32919
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;49-65/Region: complementarity-determining 2

Query Match 93.2%; Score 82; DB 2; Length 98;
Best Local Similarity 88.2%; Pred. No. 7.5e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKVG 17
:|||||
Db 50 VISYDGSNKYYADSVKVG 66

RESULT 4
S29546
Ig heavy chain V region (COS-8 / DP-46) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-Jan-1994 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C;Accession: S29546; S26888
R;Tomlinson, M.; Walter, G.; Cook, G.P.; Winter, G.
submitted to the EMBL Data Library, October 1992
A;Reference number: S29543
A;Accession: S29546
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: EMBL:Z17394; NID:g32843; PIDN:CAA78997.1; PID:g32844
A;Note: designated COS-8
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26888
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TO2>
A;Cross-references: EMBL:Z12346; NID:g32912; PIDN:CAA78216.1; PID:g32913
A;Note: designated DP-46
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 98;

Best Local Similarity 88.2%; Pred. No. 7.5e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKVG 17
:|||||
Db 50 VISYDGSNKYYADSVKVG 66

RESULT 5
PH1646
Ig heavy chain V region (clone 6H12) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C;Accession: PH1646
R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphyloc
A;Reference number: PH1642; MUID:93301610; PMID:8315388
A;Accession: PH1646
A;Molecule type: mRNA
A;Residues: 1-109 <HIL>
A;Cross-references: UNIPROT:O8WUK1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 109;
Best Local Similarity 88.2%; Pred. No. 8.4e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKVG 17
:|||||
Db 42 VISYDGSNKYYADSVKVG 58

RESULT 6
PH1644
Ig heavy chain V region (clone 5D11) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C;Accession: PH1644
R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphyloc
A;Reference number: PH1642; MUID:93301610; PMID:8315388
A;Accession: PH1644
A;Molecule type: mRNA
A;Residues: 1-109 <HIL>
A;Cross-references: UNIPROT:Q9UL93
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 109;
Best Local Similarity 88.2%; Pred. No. 8.4e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKVG 17
:|||||
Db 42 VISYDGSNKYYADSVKVG 58

RESULT 7
PH1643
Ig heavy chain V region (clone 6H7) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C;Accession: PH1643
R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphyloc
A;Reference number: PH1642; MUID:93301610; PMID:8315388
A;Accession: PH1643

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A:Molecule type: mRNA
A:Residues: 1-111 <HIL>
A:Cross-references: UNIPROT:O8WUK1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match      93.2%; Score 82; DB 2; Length 111;
Best Local Similarity 88.2%; Pred. No. 8.6e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 IISYDGSKKYYADSVKG 17
Db      42 VISYDGSNKYYADSVKG 58

RESULT 8
PH1645
Ig heavy chain V region (clone 6C8) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C:Accession: PH1645
R:Hillary, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A
A:Reference number: PH1642; MUID:93301610; PMID:8315388
A:Accession: PH1645
A:Molecule type: mRNA
A:Residues: 1-111 <HIL>
A:Cross-references: UNIPROT:O8WUK1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match      93.2%; Score 82; DB 2; Length 111;
Best Local Similarity 88.2%; Pred. No. 8.6e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 IISYDGSKKYYADSVKG 17
Db      42 VISYDGSNKYYADSVKG 58

RESULT 9
S38490
Ig heavy chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S38490
R:Marks, J.D.; Owehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S.
submitted to the EMBL Data Library, June 1993
A:Description: Human antibody fragments specific for human blood group antigens from a phage display library
A:Reference number: S38488
A:Accession: S38490
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-113 <MAR>
A:Cross-references: EMBL:Z23030; NID:9414027; PIDN:CAA80565.1; PID:G414028
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      93.2%; Score 82; DB 2; Length 113;
Best Local Similarity 88.2%; Pred. No. 8.7e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 IISYDGSKKYYADSVKG 17
Db      50 VISYDGSNKYYADSVKG 66

RESULT 10
S46390
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C:Accession: S46390
R:Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A:Title: In vitro assembly of repertoires of antibody chains on the surface of phage by a phage display library
A:Reference number: S46390; MUID:94254092; PMID:8196048
A:Accession: S46390
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-114 <FIG>
A:Cross-references: EMBL:Z31686; NID:9509782; PIDN:CAA83491.1; PID:gl3335143
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      93.2%; Score 82; DB 2; Length 114;
Best Local Similarity 88.2%; Pred. No. 8.8e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 IISYDGSKKYYADSVKG 17
Db      50 VISYDGSNKYYADSVKG 66

RESULT 11
S46392
Ig heavy chain V region (VH-28) - human
C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C:Accession: S46392
R:Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A:Title: In vitro assembly of repertoires of antibody chains on the surface of phage by a phage display library
A:Reference number: S46390; MUID:94254092; PMID:8196048
A:Accession: S46392
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-114 <FIG>
A:Cross-references: EMBL:Z31688; NID:9499306; PIDN:CAA83493.1; PID:gl3335145
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      93.2%; Score 82; DB 2; Length 114;
Best Local Similarity 88.2%; Pred. No. 8.8e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 IISYDGSKKYYADSVKG 17
Db      50 VISYDGSNKYYADSVKG 66

RESULT 12
S36270
Ig heavy chain V region (clone alpha-TNF-E1) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C:Accession: S36270
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.;
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; MUID:93178448; PMID:7679990
A:Accession: S36270
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-117 <GRI>
A:Cross-references: EMBL:Z18839; NID:933118; PIDN:CAA79291.1; PID:g939898
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>
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A:Molecule type: mRNA
A:Residues: 1-111 <HIL>
A:Cross-references: UNIPROT:O8WUK1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match      93.2%; Score 82; DB 2; Length 111;
Best Local Similarity 88.2%; Pred. No. 8.6e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 IISYDGSKKYYADSVKG 17
Db      42 VISYDGSNKYYADSVKG 58

RESULT 8
PH1645
Ig heavy chain V region (clone 6C8) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C:Accession: PH1645
R:Hillary, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A
A:Reference number: PH1642; MUID:93301610; PMID:8315388
A:Accession: PH1645
A:Molecule type: mRNA
A:Residues: 1-111 <HIL>
A:Cross-references: UNIPROT:O8WUK1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match      93.2%; Score 82; DB 2; Length 111;
Best Local Similarity 88.2%; Pred. No. 8.6e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 IISYDGSKKYYADSVKG 17
Db      42 VISYDGSNKYYADSVKG 58

RESULT 9
S38490
Ig heavy chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S38490
R:Marks, J.D.; Owehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S.
submitted to the EMBL Data Library, June 1993
A:Description: Human antibody fragments specific for human blood group antigens from a phage display library
A:Reference number: S38488
A:Accession: S38490
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-113 <MAR>
A:Cross-references: EMBL:Z23030; NID:9414027; PIDN:CAA80565.1; PID:G414028
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      93.2%; Score 82; DB 2; Length 113;
Best Local Similarity 88.2%; Pred. No. 8.7e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 IISYDGSKKYYADSVKG 17
Db      50 VISYDGSNKYYADSVKG 66

RESULT 10
S46390
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C:Accession: S46390
R:Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A:Title: In vitro assembly of repertoires of antibody chains on the surface of phage by a phage display library
A:Reference number: S46390; MUID:94254092; PMID:8196048
A:Accession: S46390
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-114 <FIG>
A:Cross-references: EMBL:Z31686; NID:9509782; PIDN:CAA83491.1; PID:gl3335143
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      93.2%; Score 82; DB 2; Length 114;
Best Local Similarity 88.2%; Pred. No. 8.8e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 IISYDGSKKYYADSVKG 17
Db      50 VISYDGSNKYYADSVKG 66

RESULT 11
S46392
Ig heavy chain V region (VH-28) - human
C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C:Accession: S46392
R:Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A:Title: In vitro assembly of repertoires of antibody chains on the surface of phage by a phage display library
A:Reference number: S46390; MUID:94254092; PMID:8196048
A:Accession: S46392
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-114 <FIG>
A:Cross-references: EMBL:Z31688; NID:9499306; PIDN:CAA83493.1; PID:gl3335145
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      93.2%; Score 82; DB 2; Length 114;
Best Local Similarity 88.2%; Pred. No. 8.8e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 IISYDGSKKYYADSVKG 17
Db      50 VISYDGSNKYYADSVKG 66

RESULT 12
S36270
Ig heavy chain V region (clone alpha-TNF-E1) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C:Accession: S36270
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.;
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; MUID:93178448; PMID:7679990
A:Accession: S36270
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-117 <GRI>
A:Cross-references: EMBL:Z18839; NID:933118; PIDN:CAA79291.1; PID:g939898
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>
```

```
Query Match      93.2%; Score 82; DB 2; Length 117;
Best Local Similarity 88.2%; Pred. No. 9e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:||||| |||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 13
S31677
Ig heavy chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31677
R/Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelle, C.
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
submitted to the EMBL Data Library, June 1992
C/Superfamily: immunoglobulin V region; immunoglobulin homology
A/Reference number: S31585
A/Accession: S31677
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-118 <CUI>
A/Cross-references: EMBL:Z14172; NID:G31009; PIDN:CAA78541.1; PID:G31010
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match      93.2%; Score 82; DB 2; Length 118;
Best Local Similarity 88.2%; Pred. No. 9.1e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:||||| |||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 14
S31116
Ig heavy chain - human
C/Species: Homo sapiens (man)
C/Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C/Accession: S31116
R/Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement
A/Reference number: S31104; MUID:9211633; PMID:173252
A/Accession: S31116
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: mRNA
A/Residues: 1-118 <RAA>
A/Cross-references: UNIPROT:Q8WUK1; EMBL:X62966
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match      93.2%; Score 82; DB 2; Length 118;
Best Local Similarity 88.2%; Pred. No. 9.1e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:||||| |||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 15
F36005
Ig heavy chain V region (M49) - human
C/Species: Homo sapiens (man)
C/Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 09-Jul-2004
C/Accession: F36005
R/Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
```

```
A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A/Reference number: A36005; MUID:90349571; PMID:2117273
A/Accession: F36005
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-119 <SCH>
A/Cross-references: UNIPROT:Q8WUK1; GB:M34026
C/Genetics:
A/Gene: GDB:IGH@; IGHDI1
A/Cross-references: GDB:118731; OMIM:146910
A/Map position: 14q32.33-14q32.33
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match      93.2%; Score 82; DB 2; Length 119;
Best Local Similarity 88.2%; Pred. No. 9.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:||||| |||||
Db 50 VISYDGSNKYYADSVKG 66

Search completed: October 14, 2005, 16:23:36
Job time : 24.6406 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 14, 2005, 15:51:44 ; Search time 113.156 Seconds
(without alignments)
76.932 Million cell updates/sec

Title: US-10-614-959-11
Perfect score: 88
Sequence: 1 IISYDGSKKYYADSVKG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	82	93.2	116	2 Q9UL93	Q9ul93 homo sapien
2	82	93.2	240	2 Q65ZC9	Q65zc9 homo sapien
3	82	93.2	613	2 Q8WUK1	Q8wuk1 homo sapien
4	74	84.1	113	2 Q9UL90	Q9ul90 homo sapien
5	74	84.1	122	1 HV3G_HUMAN	P01768 homo sapien
6	71	80.7	417	2 Q6N093	Q6n093 homo sapien
7	70	79.5	493	2 Q68CN4	Q68cn4 homo sapien
8	69	78.4	147	2 Q9Y509	Q9y509 homo sapien
9	67	76.1	482	2 Q7Z351	Q7z351 homo sapien
10	67	76.1	493	2 Q8NCL6	Q8nc16 homo sapien
11	66	75.0	122	2 Q9UL84	Q9ul84 homo sapien
12	65	73.9	119	1 HV3L_HUMAN	P01773 homo sapien
13	64	72.7	95	2 Q9ULB6	Q9ulb6 homo sapien
14	64	72.7	122	1 HV3H_HUMAN	P01769 homo sapien
15	64	72.7	470	2 Q8FJA4	Q8fpja4 homo sapien
16	64	72.7	478	2 Q6PI81	Q6pi81 homo sapien
17	63	71.6	119	1 HV3I_HUMAN	P01770 homo sapien
18	63	71.6	614	2 Q6DDQ7	Q6ddq7 xenopus lae
19	62	70.5	121	1 HV3J_HUMAN	P01771 homo sapien
20	62	70.5	519	2 Q6N092	Q6n092 homo sapien
21	61	69.3	121	2 Q9UL71	Q9ul71 homo sapien
22	61	69.3	544	2 Q6PJ95	Q6pj95 homo sapien
23	60	68.2	118	2 Q9UL72	Q9ul72 homo sapien
24	56	63.6	116	1 HV05_CARAU	P19181 carassius a
25	56	63.6	126	1 HV3K_HUMAN	P01772 homo sapien
26	56	63.6	593	2 Q6INR5	Q6inm5 xenopus lae
27	55	62.5	481	2 Q6N097	Q6n097 homo sapien
28	53	60.2	464	2 Q6MZU6	Q6mzu6 homo sapien
29	53	60.2	597	2 Q96BB9	Q96bb9 homo sapien
30	52.5	59.7	122	1 HV3A_HUMAN	P01762 homo sapien
31	52	59.1	115	1 HV3F_HUMAN	P01767 homo sapien

32	52	59.1	466	2 Q6IN78	Q6in78 homo sapien
33	52	59.1	475	2 Q6MZQ6	Q6mzq6 homo sapien
34	52	59.1	493	2 Q6GNX2	Q6gnx2 homo sapien
35	50	56.8	114	1 HV3B_HUMAN	P01763 homo sapien
36	50	56.8	119	2 Q920E7	Q920e7 mus musculus
37	50	56.8	196	2 Q65ZL8	Q65zl8 mus musculus
38	50	56.8	585	2 Q6GPX4	Q6gpx4 xenopus lae
39	49	55.7	71	2 Q9GU71	Q9gu71 salmo trutt
40	49	55.7	87	2 Q9AV03	Q9av03 oryza sativ
41	49	55.7	98	1 HV57_MOUSE	P18528 mus musculus
42	49	55.7	117	1 HV3C_HUMAN	P01764 homo sapien
43	49	55.7	480	2 Q6N094	Q6n094 homo sapien
44	49	55.7	1048	1 YC81_METJA	Q58577 methanococc
45	48.5	55.1	247	2 Q9VZF9	Q9vzf9 drosophila

ALIGNMENTS

RESULT 1		PRELIMINARY;		PRT; 116 AA.	
Q9UL93		AC Q9UL93			
DT		DT 01-MAY-2000 (Tremblrel. 13, Created)			
DT		DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)			
DT		DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)			
DE		Myosin-reactive immunoglobulin heavy chain variable region (Fragment).			
OS		Homo sapiens (Human).			
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX		NCBI_TaxID=9606;			
RN		[1]			
RP		SEQUENCE FROM N.A.			
RX		MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;			
RA		Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,			
RA		Young D.C.;			
RT		"Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."			
RL		Clin. Immunol. Immunopathol. 87:184-192(1998).			
DR		EMBL; AF035021; AAD56257.1; --			
DR		PIR; PH1644; PH1644.			
DR		PIR; PLO120; PLO120.			
DR		HSP; P01772; 2FB4.			
DR		InterPro; IPR007110; Ig-like.			
DR		InterPro; IPR003596; IG_v.			
DR		SMART; SM00406; IG; 1_			
DR		PROSITE; PS50835; IG_LIKE; 1.			
FT		NON_TER 1_1			
FT		NON_TER 116 116			
SQ		SEQUENCE 116 AA; 12434 MW; ODA0348154DB6061 CRC64;			
Query Match		93.2%; Score 82; DB 2; Length 116;			
Best Local Similarity		88.2%; Pred. No. 1e-05;			
Matches		15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;			
QY		1 IISYDGSKKYYADSVKG 17			
Db		49 VISYDGSKKYYADSVKG 65			
RESULT 2		PRELIMINARY;		PRT; 240 AA.	
Q65ZC9		ID Q65ZC9			
AC		Q65ZC9			
DT		DT 25-OCT-2004 (Tremblrel. 28, Created)			
DT		DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)			
DT		DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)			
DE		Single-chain Fv (Fragment).			
GN		Name=scFv;			
OS		Homo sapiens (Human).			
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			

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OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C1q/7;
RX MEDLINE=97362799; PubMed=9219263;
RA Kontermann R.E., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL; Y13056; CAA73499.1; -.
DR InterPro; IPR003599; Ig_Like.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER 1
FT NON_TER 240
SQ SEQUENCE 240 AA; 25569 MW; PDCFD3645F64B373 CRC64;

Query Match 93.2%; Score 82; DB 2; Length 240;
Best Local Similarity 88.2%; Pred. No. 2.3e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
Db 50 VISYDGSNKYYADSVKG 66

RESULT 3
Q8WUK1 PRELIMINARY; PRT; 613 AA.
ID Q8WUK1
AC Q8WUK1
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020240; AAH20240.1; -.
DR PIR; F36005; F36005.
DR PIR; G36005; G36005.
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DR PIR; PH1642; PH1642.
DR PIR; PH1643; PH1643.
DR PIR; PH1645; PH1645.
DR PIR; PH1646; PH1646.
DR PIR; PL0098; PL0098.
DR PIR; PL0120; PL0120.
DR PIR; S15590; S15590.
DR PIR; S31116; S31116.
DR PIR; S31119; S31119.
DR PIR; S70442; S70442.
DR HSP; P01861; IADQ.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 613 AA; 67295 MW; 60C7F5950671E315 CRC64;

Query Match 93.2%; Score 82; DB 2; Length 613;
Best Local Similarity 88.2%; Pred. No. 6.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
Db 69 VISYDGSNKYYADSVKG 85

RESULT 4
Q9UL90 PRELIMINARY; PRT; 113 AA.
ID Q9UL90
AC Q9UL90
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAY-2004 (TRENBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035024; AAD56260.1; -.
DR PIR; S78486; S78486.
DR HSP; P01772; 2FB4.
DR InterPro; IPR007110; Ig_Like.
DR SMART; SM003596; Ig_v.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12437 MW; ED57DD19086D07F CRC64;

Query Match 84.1%; Score 74; DB 2; Length 113;
Best Local Similarity 87.5%; Pred. No. 0.00022;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 IISYDGSKKYYADSVKG 17
Db 51 IRYDGSNKYYADSVKG 66

RESULT 5
HV3G HUMAN
ID HV3G HUMAN STANDARD; PRT; 122 AA.
AC P01768;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
```

05-JUL-2004 (Rel. 44, Last annotation update)
Ig heavy chain V-III region CAM.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE.
MEDLINE=81013859; PubMed=6774332;
Lehman D.W., Putnam F.W.;
"Amino acid sequence of the variable region of a human mu chain:
location of a possible JH segment.";
Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
-!- MISCELLANEOUS: This mu chain was isolated from the plasma of a
patient with macroglobulinemia.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A02051; M3HUM.
HSSP; P01772; 2FB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; IG-like.
InterPro; IPR003596; IG_v.
Pfam; PF00047; IG; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin V region;
Pyrolydione carboxylic acid.
DOMAIN 1 112 IG-like.
MOD_RES 1 122 Pyrolydione carboxylic acid.
NON_TER 122 122
SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;
Query Match 84.1%; Score 74; DB 1; Length 122;
Best Local Similarity 70.6%; Pred. No. 0.00024;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 1 IISYDGSKKYADSVKG 17
Db 50 VISYEGBKRYABSVKG 66
RESULT 6
Q6N093 PRELIMINARY; PRT; 417 AA.
AC Q6N093;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKF2686I04196;
GN Name=DKF2686I04196;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
TISSUE=Human esophagus tumor;
The German Human cDNA Consortium;
Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
Fobo G., Han M., Wiemann S.;
Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
EMBL; BX640623; CAB45777.1;
HSSP; P01861; IADQ.
InterPro; IPR003599; IG.
InterPro; IPR007110; IG-like.
InterPro; IPR003597; IG cl.
InterPro; IPR003006; IG_MHC.
InterPro; IPR003596; IG_v.
Pfam; PF07654; Cl-set; 3.
SMART; SM00409; IG; 2.
SMART; SM00407; IGV; 1.
SEQUENCE 493 AA; 54117 MW; A1E4F5ED3F8AB40 CRC64;
Query Match 79.5%; Score 70; DB 2; Length 493;
Best Local Similarity 70.6%; Pred. No. 0.0052;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
Qy 1 IISYDGSKKYADSVKG 17
Db 92 VISYEGKQHYADSVKG 108
RESULT 8
Q9Y509 PRELIMINARY; PRT; 147 AA.
ID Q9Y509
AC Q9Y509;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VH3 protein (Fragment).
GN Name=VH3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

DR PROSITE; PS50835; IG LIKE; 3.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 417 AA; 46061 MW; C4518EB844CFB883C CRC64;
Query Match 80.7%; Score 71; DB 2; Length 417;
Best Local Similarity 70.6%; Pred. No. 0.0029;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
Qy 1 IISYDGSKKYADSVKG 17
Db 22 VIAYDGSQYYADSVRG 38
RESULT 7
Q68CN4 PRELIMINARY; PRT; 493 AA.
ID Q68CN4
AC Q68CN4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein DKF2686E23209;
GN Name=DKF2686E23209;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
TISSUE=Rectum tumor;
The German cDNA Consortium;
Bloecker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,
Osanger A., Fobo G., Han M., Wiemann S.;
Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
EMBL; CR749861; CAH18705.1;
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
Pfam; PF07654; Cl-set; 3.
Pfam; PF00047; IG; 4.
SMART; SM00409; IG; 2.
SMART; SM00407; IGV; 3.
SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 493 AA; 54117 MW; A1E4F5ED3F8AB40 CRC64;
Query Match 79.5%; Score 70; DB 2; Length 493;
Best Local Similarity 70.6%; Pred. No. 0.0052;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
Qy 1 IISYDGSKKYADSVKG 17
Db 92 VISYEGKQHYADSVKG 108
RESULT 8
Q9Y509 PRELIMINARY; PRT; 147 AA.
ID Q9Y509
AC Q9Y509;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VH3 protein (Fragment).
GN Name=VH3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96071149; PubMed=7475288;
RZ Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
RA Lichtenstein A.K., Berenson J.R.;
RT "A CD10-positive subset of malignant cells is identified in multiple
RT myeloma using PCR with patient-specific immunoglobulin gene primers.";
RL Leukemia 9:1948-1953(1995).
DR EMBL; S80860; AAD14339.1; -.
DR HSSP; P01842; 1AOK.
DR GO; GO:0005887; C:integral to plasma membrane; NAS.
DR GO; GO:0016066; P:cellular defense response (sensu Vertebrata); NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 147
SQ SEQUENCE 147 AA; 15768 MW; 8489FCAAA7BC925C CRC64;

Query Match 78.4%; Score 69; DB 2; Length 147;
Best Local Similarity 76.5%; Pred. No. 0.002;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 IISYDGSKYYADSVKG 17
Db :|||||:|||||
50 LISYDGSQTQYAGSVKG 66

RESULT 9
Q72351 PRELIMINARY; PRT; 482 AA.
ID Q72351
AC Q72351;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp686N02209.
GN Name=DKFZp686N02209;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Human rectum tumor;
RA Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX538118; CAD98026.1; -.
DR HSSP; P01857; 1H2H.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 482 AA; 52852 MW; EDA75F1901D1A034 CRC64;

Query Match 76.1%; Score 67; DB 2; Length 482;
Best Local Similarity 70.6%; Pred. No. 0.016;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 IISYDGSKYYADSVKG 17
Db :|||||:|||||
69 VISYDGNHKLVSQSVKG 85

RESULT 10
Q8NCL6 PRELIMINARY; PRT; 493 AA.
ID Q8NCL6

```

```

AC Q8NCL6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein FLJ90170.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Mammary gland;
RA Isoqai T., Ota T., Nishikawa T., Hayaashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK074651; BAC11114.1; -.
DR HSSP; P01876; 1OWO.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 493 AA; 53224 MW; 12ECD7B094777101 CRC64;

Query Match 76.1%; Score 67; DB 2; Length 493;
Best Local Similarity 70.6%; Pred. No. 0.016;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 IISYDGSKYYADSVKG 17
Db :|||||:|||||
69 LIWYDGTQYSDSVKG 85

RESULT 11
Q9UL84 PRELIMINARY; PRT; 122 AA.
ID Q9UL84
AC Q9UL84;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RX Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035030; AAD56266.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 122
SQ SEQUENCE 122 AA; 13579 MW; 36054D4136545B8 CRC64;

Query Match 75.0%; Score 66; DB 2; Length 122;
Best Local Similarity 81.2%; Pred. No. 0.0053;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```


QY 2 ISYDGSKKYYADSVKG 17
 DB 51 ISNDGSKFYADSVKG 66

RESULT 12
 HV3L HUMAN STANDARD; PRT; 119 AA.
 ID HV3L HUMAN
 AC P01773;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig heavy chain V-III region BUR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE (MYELOMA PROTEIN BUR).
 RX MEDLINE=79151016; PubMed=107164;
 RA Putnam P.W., Liu Y.-S.V., Low T.L.K.;
 RT "Primary structure of a human IgA1 immunoglobulin. IV. Streptococcal
 RT IgA1 protease, digestion, Fab and Fc fragments, and the complete amino
 RT acid sequence of the alpha 1 heavy chain.";
 RL J. Biol. Chem. 254:2865-2874 (1979).
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A02056; A1HUBR.
 DR HSSP; P01772; 2FB4.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-Like.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR Direct protein sequencing; Immunoglobulin V region;
 DR Pyroliidone carboxylic acid.
 FT MOD_RES 1 112
 FT DISULFID 22 96
 FT CARBOHYD 28 28
 FT NON_TER 119 119
 FT N-linked (GlcNAc. . .).
 SQ SEQUENCE 119 AA; 12981 MW; 12A709A7534D024 CRC64;

Query Match 73.9%; Score 65; DB 1; Length 119;
 Best Local Similarity 70.6%; Pred. No. 0.0076;
 Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
 DB 50 LISYGSSTYYADSVRG 66

RESULT 13
 Q9ULB6 PRELIMINARY; PRT; 95 AA.
 ID Q9ULB6
 AC Q9ULB6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Immunoglobulin heavy chain (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tange Y., Kayano H.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB03268; BAA87067.1; -.
 DR PIR; PH0872; PH0872.

DR PIR; S36280; S36280.
 DR HSSP; P01820; IG7J.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_V.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 FT NON_TER 1 95
 FT NON_TER 95 95
 SQ SEQUENCE 95 AA; 10527 MW; 90A8C6D16D22574A CRC64;

Query Match 72.7%; Score 64; DB 2; Length 95;
 Best Local Similarity 75.0%; Pred. No. 0.0087;
 Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 ISYDGSKKYYADSVKG 17
 DB 50 IKQDGSKKYYADSVKG 65

RESULT 14
 HV3H HUMAN STANDARD; PRT; 122 AA.
 ID HV3H HUMAN
 AC P01769;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig heavy chain V-III region GA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=74175307; PubMed=4208843;
 RA Florent G., Lehman D., Putnam P.W.;
 RT "The switch point in mu heavy chains of human IGM immunoglobulins.";
 RL Biochemistry 13:2482-2498 (1974).
 CC -!- MISCELLANEOUS: This chain was isolated from a Waldenstrom's
 CC macroglobulin.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A02052; M3HUGA.
 DR HSSP; P01772; 2FB4.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-Like.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR Direct protein sequencing; Immunoglobulin V region;
 DR Pyroliidone carboxylic acid.
 FT MOD_RES 1 112
 FT NON_TER 122 122
 FT Pyroliidone carboxylic acid.
 SQ SEQUENCE 122 AA; 13166 MW; 74E5B6959E84100A CRC64;

Query Match 72.7%; Score 64; DB 1; Length 122;
 Best Local Similarity 64.7%; Pred. No. 0.011;
 Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
 DB 50 VISYGBBZYAAASVKG 66

RESULT 15
 Q6PJA4 PRELIMINARY; PRT; 470 AA.
 ID Q6PJA4
 AC Q6PJA4;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

Query Match	72.7%;	Score 64;	DB 2;	Length 470;
Best Local Similarity	75.0%;	Pred. No. 0.05;		
Matches 12: Conservative	1: Mismatches	3: Indels	0: Gaps	0:

Search completed: October 14, 2005, 16:19:51
Job time : 115.156 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2005, 15:51:19 ; Search time 84.5625 Seconds
(without alignments)
50.310 Million cell updates/sec

Title: US-10-614-959-12
Perfect score: 50
Sequence: 1 ASIAAARVLDY 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	100.0	11	3	AAY79070 Anti-fact
2	46	92.0	11	3	AAY79077 Anti-fact
3	37	74.0	408	8	ADJ48827 Oil-assoc
4	36	72.0	58	4	AAO13448 Human pol
5	36	72.0	652	8	ADs26132 Bacterial
6	36	72.0	652	8	ADs25655 Bacterial
7	36	72.0	655	8	ADs25373 Bacterial
8	36	72.0	656	8	ADs22602 Bacterial
9	35	70.0	708	5	ABb48560 Bacteria
10	34	68.0	157	3	AGI18510 Zea mays
11	34	68.0	159	3	AGI18509 Zea mays
12	34	68.0	180	2	AAY37904 Amino aci
13	34	68.0	231	8	ADs28058 Bacterial
14	34	68.0	237	3	AAG20306 Bacterial
15	34	68.0	237	3	AAG51887 Arabidops
16	34	68.0	278	1	AAp80850 Sequence
17	34	68.0	279	1	AAp80274 Amino aci
18	34	68.0	279	2	AAr54838 Thermitas
19	34	68.0	279	2	AAW00768 Thermitas
20	34	68.0	279	2	AAW00769 Thermitas
21	34	68.0	279	2	AAW00774 Thermitas
22	34	68.0	279	2	AAW00798 Thermitas
23	34	68.0	279	2	AAW00770 Thermitas
24	34	68.0	279	2	AAW00775 Thermitas
25	34	68.0	279	2	AAW00780 Thermitas

ALIGNMENTS

RESULT 1
AAY79070
ID AAY79070 standard; peptide; 11 AA.
XX
AC AAY79070;
XX

DT 12-JUN-2000 (first entry)
XX

DE Anti-factor IX/IXa antibody H chain V domain CDR3 amino acid sequence.
KW Complementarity determining region 3; CDR3; antibody; Gla domain;
KW factor IX/IXa; blood coagulation; deep venous thrombosis;
KW arterial thrombosis; unstable angina; post myocardial infarction;
KW coronary artery bypass graft; CABG; stroke; tumour growth; metastasis;
KW percutaneous transluminal coronary angioplasty; PTCA; inflammation;
KW septic shock; hypotension; adult respiratory distress syndrome; ARDS;
KW arterial fibrillation; disseminated intravascular coagulopathy; DIC.

OS Homo sapiens.
XX

PN WO200012562-A1.
XX

PD 09-MAR-2000.
XX

PF 26-AUG-1999; 99WO-US019453.
XX

PR 28-AUG-1998; 98US-0098233P.
03-MAR-1999; 99US-0122767P.
XX

PA (GETH) GENENTECH INC.
XX

PI Adams CW, Devaux B, Eaton DL, Hass PE, Judice JK, Kirchhofer D;
PI Suggett S;
XX

DR WPI; 2000-256595/22.
XX

PT Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-
PT carboxyglutamic acid domains useful as anti-coagulant in thrombosis,
PT stroke, and post myocardial infarction.
XX

PS Claim 2; Fig 2; 84pp; English.
XX

CC This sequence represents a complementarity determining region 3 (CDR3) of
CC the heavy chain variable domain of a human anti-factor IX/IXa Gla domain
CC antibody. Factor IXa is a vitamin K dependent plasma serine protease that
CC participates in the blood coagulation pathways. The Gla domain of factor
CC IXa and its zymogen factor IX contains important structural determinants
CC for interaction with high affinity binding sites on vascular endothelial

Aaw00783 Thermitas
Aaw00792 Thermitas
Aaw00772 Thermitas
Aaw00784 Thermitas
Aaw00793 Thermitas
Aaw00796 Thermitas
Aaw00794 Thermitas
Aaw00776 Thermitas
Aaw00785 Thermitas
Aaw00787 Thermitas
Aaw00789 Thermitas
Aaw00799 Thermitas
Aaw00803 Thermitas
Aaw00767 Thermitas
Aaw00771 Thermitas
Aaw00801 Thermitas
Aaw00790 Thermitas
Aaw00788 Thermitas
Aaw00797 Thermitas
Aaw00800 Thermitas

CC cells and platelets. Compositions comprising the antibodies are used for
CC the treatment or prophylaxis of thrombotic or coagulopathic diseases or
CC disorders in a mammal for which inhibiting a FIX/Ixa mediated event is
CC indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable
CC angina, post myocardial infarction, post surgical thrombosis, coronary
CC artery bypass graft (CABG), percutaneous transluminal coronary
CC angioplasty (PTCA), stroke, tumour growth, invasion or metastasis,
CC inflammation, septic shock, hypotension, adult respiratory distress
CC syndrome (ARDS), arterial fibrillation and disseminated intravascular
CC coagulopathy (DIC)
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 50; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTAAARVLDY 11
DB 1 ASIAAARVLDY 11

RESULT 2
AAY79077
ID AAY79077 standard; peptide; 11 AA.
XX
AC
XX
XX
DT 12-JUN-2000 (first entry)
XX
DE Anti-factor IX/Ixa antibody H chain V domain CDR3 amino acid sequence.
XX
KW Complementarity determining region 3; CDR3; antibody; Gla domain;
KW factor IX/Ixa; blood coagulation; deep venous thrombosis;
KW arterial thrombosis; unstable angina; post myocardial infarction;
KW coronary artery bypass graft; CABG; stroke; tumour growth; metastasis;
KW percutaneous transluminal coronary angioplasty; PTCA; inflammation;
KW septic shock; hypotension; adult respiratory distress syndrome; ARDS;
KW arterial fibrillation; disseminated intravascular coagulopathy; DIC.
XX
OS Homo sapiens.
XX
XX WO200012562-A1.
XX
PD 09-MAR-2000.
XX
XX 26-AUG-1999; 99WO-US019453.
XX
XX 28-AUG-1998; 98US-0098233P.
XX
XX 03-MAR-1999; 99US-0122767F.
XX
XX (GETH) GENENTECH INC.
XX
XX Adams CW, Devaux B, Eaton DL, Hass PE, Judice JK, Kirchhofer D;
XX Suggett S;
XX
XX WPI; 2000-256595/22.
XX
XX Novel human anti-Factor IX/Ixa antibodies against IX/Ixa gamma-
XX carboxylglutamic acid domains useful as anti-coagulant in thrombosis,
XX stroke, and post myocardial infarction.
XX
XX Claim 2; Fig 2; 84pp; English.
XX
XX This sequence represents a complementarity determining region 3 (CDR3) of
XX the heavy chain variable domain of a human anti-factor IX/Ixa Gla domain
XX antibody. Factor IXa is a vitamin K dependent plasma serine protease that
XX participates in the blood coagulation pathways. The Gla domain of factor
XX IXa and its zymogen factor IX contains important structural determinants
XX for interaction with high affinity binding sites on vascular endothelial
XX cells and platelets. Compositions comprising the antibodies are used for
XX the treatment or prophylaxis of thrombotic or coagulopathic diseases or
XX disorders in a mammal for which inhibiting a FIX/Ixa mediated event is

CC indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable
CC angina, post myocardial infarction, post surgical thrombosis, coronary
CC artery bypass graft (CABG), percutaneous transluminal coronary
CC angioplasty (PTCA), stroke, tumour growth, invasion or metastasis,
CC inflammation, septic shock, hypotension, adult respiratory distress
CC syndrome (ARDS), arterial fibrillation and disseminated intravascular
CC coagulopathy (DIC)
XX
SQ Sequence 11 AA;

Query Match 92.0%; Score 46; DB 3; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASTAAARVLDY 11
DB 1 ASIAAGRVLVDY 11

RESULT 3
ADJ48827
ID ADJ48827 standard; protein; 408 AA.
XX
AC
XX
XX
DT 06-MAY-2004 (first entry)
XX
DE Oil-associated gene related protein #327.
XX
KW oil-associated gene; transgenic; enhanced seed oil; vegetable oil.
XX
OS Unidentified.
XX
XX US2004025202-A1.
XX
XX 05-FEB-2004.
XX
XX 14-MAR-2003; 2003US-00389566.
XX
XX 15-MAR-2002; 2002US-0365301P.
XX
XX 26-JUN-2002; 2002US-0391786P.
XX
XX 26-JUN-2002; 2002US-0392018P.
XX
XX (LAUR/) LAURIE C C.
XX (RAVA/) RAVANELLO M.
XX (SAVA/) SAVAGE T.
XX (LEDE/) LEDEAUX J R.
XX (ROGE/) ROGERS J A.
XX
XX Laurie CC, Ravanello M, Savage T, Ledeaux JR, Rogers JA;
XX
XX WPI; 2004-142683/14.
XX
XX Novel recombinant DNA construct comprising a promoter functional in
XX plants operably linked to an oil-associated gene for producing transgenic
XX plant seed.
XX
XX Example 3; SEQ ID NO 831; 22pp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a
XX promoter functional in plants operably linked to an oil-associated gene.
XX The construct is useful for transgenic plant seed which has in its genome
XX the construct, that is functional in the plant to transcribe the oil-
XX associated gene. The transgenic plant seed grows into a plant having
XX enhanced seed oil as compared to wild type. The construct is useful for
XX producing hybrid maize seed. The transgenic plant seed is useful for
XX producing vegetable oil. The present sequence represents the amino acid
XX sequence of an oil-associated gene related protein.
XX
XX Sequence 408 AA;

Query Match 74.0%; Score 37; DB 8; Length 408;
Best Local Similarity 80.0%; Pred. No. 62;

```
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 ASIAARVLD 10
DB 275 ASIAARALD 284

RESULT 4
AAOL3448
ID AAOL3448 standard; protein; 58 AA.
AC AAOL3448;
XX
XX 06-NOV-2001 (first entry)
XX
XX Human polypeptide SEQ ID NO 27340.
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX
XX Homo sapiens.
XX
XX WO200164835-A2.
XX
XX 07-SEP-2001.
XX
XX 26-FEB-2001; 2001WO-US004927.
XX
XX 28-FEB-2000; 2000US-00515126.
XX
XX 18-MAY-2000; 2000US-00577409.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX
XX WPI; 2001-514838/56.
XX
XX N-FSDB; AA193379.
XX
XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
XX and treating e.g. leukemia, inflammation and immune disorders.
XX
XX Claim 20; SEQ ID NO 27340; 1399pp + Sequence Listing; English.
XX
XX The invention relates to human polynucleotides (AA179941-AA193841) and
XX the encoded proteins (AAO0010-AAO13910) that exhibit activity relating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoiesis regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activin/inhibin activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX inflammation. Note: The sequence data for this patent did not form part
XX of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 58 AA;
XX
XX Query Match 72.0%; Score 36; DB 4; Length 58;
XX Best Local Similarity 70.0%; Pred. No. 12;
XX Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX
XX 2 SIAAARVLDY 11
XX
XX 12 SVAQARVLEY 21
XX
XX RESULT 5
XX ADS26132
XX ID ADS26132 standard; protein; 652 AA.
```

```
XX ADS26132;
XX
XX 02-DEC-2004 (first entry)
XX
XX Bacterial polypeptide #15165.
XX
XX Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
XX Bacteria.
XX
XX US2003233675-A1.
XX
XX 18-DEC-2003.
XX
XX 20-FEB-2003; 2003US-00369493.
XX
XX 21-FEB-2002; 2002US-0360039P.
XX
XX (CAOY/) CAO Y.
XX (HINK/) HINKLE G J.
XX (SLAT/) SLATER S C.
XX (CHEN/) CHEN X.
XX (GOLD/) GOLDMAN B S.
XX
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
XX for expression of a polynucleotide encoding a polypeptide from a
XX microbial source, useful for producing plants with improved properties.
XX
XX Claim 1; SEQ ID NO 15165; 122pp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a
XX promoter functional in a plant cell, where the promoter is positioned to
XX provide for expression of a polynucleotide encoding a polypeptide from a
XX microbial source. The invention also relates to a transformed plant
XX comprising the recombinant DNA construct and a method of producing a
XX transformed plant having an improved property. The plant is a crop plant
XX such as maize or soybean. The method of producing a transformed plant
XX having an improved property comprises transforming a plant with the
XX recombinant DNA construct and growing the transformed plant, where the
XX polynucleotide or polypeptide is useful for improving plant properties.
XX The recombinant DNA construct is useful for producing plants with
XX improved plant properties, e.g. improved cold, heat or drought tolerance,
XX tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
XX increased resistance to plant disease, better growth rate by modification
XX of the cell cycle pathway with plant growth regulators, increased rate of
XX homologous recombination, modified seed oil or protein yield and/or
XX content, improved yield by modification of carbohydrate, nitrogen or
XX phosphorus use and/or uptake, by modification of photosynthesis or by
XX providing improved plant growth and development under at least one stress
XX condition, improved lignin production or improved galactomannan
XX production. This sequence represents a bacterial polypeptide used in the
XX scope of the invention. Note: The sequence data for this patent did not
XX form part of the printed specification but was obtained in electronic
XX format from USPTO at seqdata.uspto.gov/sequence.html.
XX
XX Sequence 652 AA;
XX
XX Query Match 72.0%; Score 36; DB 8; Length 652;
XX Best Local Similarity 63.6%; Pred. No. 1.6e+02;
XX Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 ASIAARVLDY 11
XX
XX QY
```

255 AATAAARAIDY 265

Sequence 652 AA;

Query Match 72.0%; Score 36; DB 8; Length 652;
Best Local Similarity 63.6%; Pred. No. 1.6e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

RESULT 6
ID ADS25655 standard; protein; 652 AA.

QY 1 ASTAAARVLDY 11
DB 255 AATAAARAIDY 265

02-DEC-2004 (first entry)

Bacterial polypeptide #14688.

Recombinant DNA construct; transformed plant; improved plant property;
cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
pathogen tolerance; pest tolerance; plant disease resistance;
cell cycle pathway modification; plant growth regulator;
homologous recombination; seed oil yield; protein yield; carbohydrate;
nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
bacterial polypeptide.

Bacteria.

US2003233675-A1.

18-DEC-2003.

20-FEB-2003; 2003US-00369493.

21-FEB-2002; 2002US-0360039P.

(CAOY/) CAO Y.
(HINK/) HINKLE G J.
(SLAT/) SLATER S C.
(CHEN/) CHEN X.
(GOLD/) GOLDMAN B S.

Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

WPI; 2004-061375/06.

New recombinant DNA construct comprising a promoter positioned to provide
for expression of a polynucleotide encoding a polypeptide from a
microbial source, useful for producing plants with improved properties.

Claim 1; SEQ ID NO 14688; 122pp; English.

The invention relates to a recombinant DNA construct comprising a
promoter functional in a plant cell, where the promoter is positioned to
provide for expression of a polynucleotide encoding a polypeptide from a
microbial source. The invention also relates to a transformed plant
comprising the recombinant DNA construct and a method of producing a
transformed plant having an improved property. The plant is a crop plant
such as maize or soybean. The method of producing a transformed plant
having an improved property comprises transforming a plant with the
recombinant DNA construct and growing the transformed plant, where the
polynucleotide or polypeptide is useful for producing plant properties.
The recombinant DNA construct is useful for producing plants with
improved plant properties, e.g. improved cold, heat or drought tolerance,
tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
increased resistance to plant disease, better growth rate by modification
of the cell cycle pathway with plant growth regulators, increased rate of
homologous recombination, modified seed oil or protein yield and/or
content, improved yield by modification of carbohydrate, nitrogen or
phosphorus use and/or uptake, by modification of photosynthesis or by
providing improved plant growth and development under at least one stress
condition, improved lignin production or improved galactomannan
production. This sequence represents a bacterial polypeptide used in the
scope of the invention. Note: The sequence data for this patent did not
form part of the printed specification but was obtained in electronic
format from USPTO at seqdata.uspto.gov/sequence.html.

RESULT 7

ID ADS25373 standard; protein; 655 AA.

AC ADS25373;

DT 02-DEC-2004 (first entry)

DE Bacterial polypeptide #14406.

Recombinant DNA construct; transformed plant; improved plant property;
cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
pathogen tolerance; pest tolerance; plant disease resistance;
cell cycle pathway modification; plant growth regulator;
homologous recombination; seed oil yield; protein yield; carbohydrate;
nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
bacterial polypeptide.

Bacteria.

US2003233675-A1.

18-DEC-2003.

20-FEB-2003; 2003US-00369493.

21-FEB-2002; 2002US-0360039P.

(CAOY/) CAO Y.
(HINK/) HINKLE G J.
(SLAT/) SLATER S C.
(CHEN/) CHEN X.
(GOLD/) GOLDMAN B S.

Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

WPI; 2004-061375/06.

New recombinant DNA construct comprising a promoter positioned to provide
for expression of a polynucleotide encoding a polypeptide from a
microbial source, useful for producing plants with improved properties.

Claim 1; SEQ ID NO 14406; 122pp; English.

The invention relates to a recombinant DNA construct comprising a
promoter functional in a plant cell, where the promoter is positioned to
provide for expression of a polynucleotide encoding a polypeptide from a
microbial source. The invention also relates to a transformed plant
comprising the recombinant DNA construct and a method of producing a
transformed plant having an improved property. The plant is a crop plant
such as maize or soybean. The method of producing a transformed plant
having an improved property comprises transforming a plant with the
recombinant DNA construct and growing the transformed plant, where the
polynucleotide or polypeptide is useful for producing plant properties.
The recombinant DNA construct is useful for producing plants with
improved plant properties, e.g. improved cold, heat or drought tolerance,
tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
increased resistance to plant disease, better growth rate by modification
of the cell cycle pathway with plant growth regulators, increased rate of
homologous recombination, modified seed oil or protein yield and/or
content, improved yield by modification of carbohydrate, nitrogen or
phosphorus use and/or uptake, by modification of photosynthesis or by

CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 655 AA;

Query Match 72.0%; Score 36; DB 8; Length 655;
Best Local Similarity 63.6%; Pred. No. 1.6e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 ASIAAARVLDY 11
|: |||| :||
Db 255 AATAAARAIDY 265

RESULT 8
ADS22602
ID ADS22602 standard; protein; 656 AA.
XX
AC ADS22602;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polypeptide #11635.
XX

KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.

XX
OS Bacteria.
XX
PN US2003233675-A1.
XX

PD 18-DEC-2003.
XX
PF 20-FEB-2003; 2003US-00369493.
XX
PR 21-FEB-2002; 2002US-0360039P.
XX

XX (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.

PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX
DR WPI; 2004-061375/06.

XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX

PS Claim 1; SEQ ID NO 11635; 122pp; English.

XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with

CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 656 AA;

Query Match 72.0%; Score 36; DB 8; Length 656;
Best Local Similarity 63.6%; Pred. No. 1.7e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 ASIAAARVLDY 11
|: |||| :||
Db 255 AATAAARAIDY 265

RESULT 9
ABB48560
ID ABB48560 standard; protein; 708 AA.

XX
AC ABB48560;

XX
DT 05-FEB-2002 (first entry)

XX
DE Listeria monocytogenes protein #1264.

XX
KW Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
KW vitamin B12; bacterial infection; disease.

XX
OS Listeria monocytogenes.

XX
PN WO200177335-A2.

XX
PD 18-OCT-2001.

XX
PF 11-APR-2001; 2001WO-FR001118.

XX
PR 11-APR-2000; 2000FR-00004629.

XX (INSP) INST PASTEUR.

XX Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P;
PI Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Coesart P;
PI Daniela J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;
PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L;
PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
PI Maduenio E, De Pablos B, Wehlend J, Kaerst U, Entian K, Hauf J;
PI Rose M, Voss H;

XX WPI; 2002-010914/01.

XX Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
PT and prevention of Listeria and related bacterial infections, and related
PT polypeptides.

XX Claim 6; SEQ ID NO 1265; 192pp; French.

XX The present invention relates to the genome sequence of Listeria
CC monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
CC it are useful for selecting probes and primers for detecting genes in L.
CC monocytogenes and related organisms, and for studying genetic
CC polymorphisms and other genomes. The present sequence is a protein
CC encoded by the genome sequence of the present invention. Proteins


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PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
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PR 13-AUG-1999; 99US-0148684P.
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PR 17-AUG-1999; 99US-0149175P.
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PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157533P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158028P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.

PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 68.0%; Score 34; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AARVLDY 11
Db 117 AARVLDY 123

RESULT 11
AAG18509
ID AAG18509 standard; protein; 159 AA.
XX
AC AAG18509;
XX
DT 17-OCT-2000 (first entry)
XX
DE Zea mays protein fragment SEQ ID NO: 19947.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.
XX
OS Zea mays subsp. mays.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
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PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 07-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
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PR 21-MAY-1999; 99US-0135353P.
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PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
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PR	28-MAY-1999;	99US-0136782P.
PR	01-JUN-1999;	99US-0137222P.
PR	03-JUN-1999;	99US-0137528P.
PR	04-JUN-1999;	99US-0137502P.
PR	07-JUN-1999;	99US-0137724P.
PR	08-JUN-1999;	99US-0138094P.
PR	10-JUN-1999;	99US-0138540P.
PR	10-JUN-1999;	99US-0138647P.
PR	14-JUN-1999;	99US-0139119P.
PR	16-JUN-1999;	99US-0139452P.
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PR	18-JUN-1999;	99US-0139455P.
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PR	18-JUN-1999;	99US-0139457P.
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PR	27-JUL-1999;	99US-0145913P.
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PR	27-JUL-1999;	99US-0145919P.
PR	28-JUL-1999;	99US-0145951P.
PR	02-AUG-1999;	99US-0146388P.
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PR	03-AUG-1999;	99US-0147038P.
PR	04-AUG-1999;	99US-0147204P.
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PR	06-AUG-1999;	99US-0147260P.
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PR	11-AUG-1999;	99US-0148319P.
PR	12-AUG-1999;	99US-0148341P.
PR	13-AUG-1999;	99US-0148565P.
PR	13-AUG-1999;	99US-0148684P.
PR	16-AUG-1999;	99US-0149368P.
PR	17-AUG-1999;	99US-0149175P.
PR	18-AUG-1999;	99US-0149426P.
PR	20-AUG-1999;	99US-0149722P.
PR	20-AUG-1999;	99US-0149723P.
PR	20-AUG-1999;	99US-0149929P.
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PR	25-AUG-1999;	99US-0150566P.
PR	26-AUG-1999;	99US-0150884P.
PR	27-AUG-1999;	99US-0151065P.
PR	27-AUG-1999;	99US-0151066P.
PR	27-AUG-1999;	99US-0151080P.
PR	30-AUG-1999;	99US-0151303P.
PR	31-AUG-1999;	99US-0151438P.
PR	01-SEP-1999;	99US-0151930P.
PR	07-SEP-1999;	99US-0152363P.
PR	10-SEP-1999;	99US-0153070P.
PR	11-SEP-1999;	99US-0153758P.
PR	16-SEP-1999;	99US-0154018P.
PR	20-SEP-1999;	99US-0154779P.
PR	22-SEP-1999;	99US-0155139P.
PR	23-SEP-1999;	99US-0155486P.
PR	24-SEP-1999;	99US-0155659P.
PR	28-SEP-1999;	99US-0156458P.
PR	29-SEP-1999;	99US-0156596P.
PR	04-OCT-1999;	99US-0157117P.
PR	05-OCT-1999;	99US-0157753P.
PR	06-OCT-1999;	99US-0157865P.
PR	07-OCT-1999;	99US-0158029P.
PR	08-OCT-1999;	99US-0158232P.
PR	12-OCT-1999;	99US-0158369P.
PR	13-OCT-1999;	99US-0159293P.
PR	13-OCT-1999;	99US-0159294P.
PR	13-OCT-1999;	99US-0159295P.
PR	14-OCT-1999;	99US-0159329P.
PR	14-OCT-1999;	99US-0159330P.
PR	14-OCT-1999;	99US-0159331P.
PR	14-OCT-1999;	99US-0159637P.
PR	14-OCT-1999;	99US-0159638P.
PR	18-OCT-1999;	99US-0159584P.
PR	21-OCT-1999;	99US-0160741P.
PR	21-OCT-1999;	99US-0160767P.
PR	21-OCT-1999;	99US-0160768P.
PR	21-OCT-1999;	99US-0160770P.
PR	21-OCT-1999;	99US-0160814P.
PR	21-OCT-1999;	99US-0160815P.
PR	22-OCT-1999;	99US-0160980P.
PR	22-OCT-1999;	99US-0160981P.
PR	22-OCT-1999;	99US-0160989P.
PR	25-OCT-1999;	99US-0161404P.
PR	25-OCT-1999;	99US-0161405P.
PR	25-OCT-1999;	99US-0161406P.
PR	26-OCT-1999;	99US-0161359P.
PR	26-OCT-1999;	99US-0161360P.
PR	26-OCT-1999;	99US-0161361P.
PR	28-OCT-1999;	99US-0161920P.
PR	28-OCT-1999;	99US-0161992P.
PR	28-OCT-1999;	99US-0161993P.
PR	29-OCT-1999;	99US-0162142P.

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Query Match      68.0%; Score 34; DB 3; Length 159;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AARVLDY 11
DB 119 AARVLDY 125

RESULT 12
AAY37904
ID AAY37904 standard; protein; 180 AA.
XX AAY37904;
AC AAY37904;
XX
XX 07-OCT-1999 (first entry)
XX
XX Amino acid sequence of a Chlamydia trachomatis protein.
XX
XX Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
KW paratrachoma; inclusion conjunctivitis; genital disease; perihhepatitis;
KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis;
KW bartholinitis; pneumopathy; venereal lymphogranulomatosis.
XX
XX Chlamydia trachomatis.
XX
XX WO9928475-A2.
XX
XX 10-JUN-1999.
XX
XX 27-NOV-1998; 98WO-IB001939.
XX
XX 28-NOV-1997; 97FR-00015041.
XX 17-DEC-1997; 97PR-00016034.
XX 04-NOV-1998; 98US-0107077P.
XX
XX (GEST ) GENSET.
XX
XX Griffais R;
XX
XX WPI; 1999-371125/31.
XX
XX Genome sequence of Chlamydia trachomatis.
XX
XX Disclosure; Page 1426; 1755pp; English.
XX
XX AAY36754-Y37949 are encoded by open reading frames (ORFs) of the genome
CC of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as
CC vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences
CC can also be used to control growth of the microorganism. Chlamydia
CC trachomatis is responsible for a large number of diseases, e.g. eye
CC diseases such as conventional trachoma, nonendemic trachoma,
CC paratrachoma, and inclusion conjunctivitis; genital diseases such as
CC nongonococcal urethritis, epididymitis, cervicitis, salpingitis, and
CC perihhepatitis, bartholinitis; pneumopathy in breast feeding infants; and
CC venereal lymphogranulomatosis. The polypeptides of the invention may be
CC of use in treating these diseases
XX
XX Sequence 180 AA;
SQ
Query Match      68.0%; Score 34; DB 2; Length 180;
Best Local Similarity 77.8%; Pred. No. 1e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 IAAARVLDY 11
DB 140 IAAARVLDY 148

RESULT 13
ADS28058
ID ADS28058 standard; protein; 231 AA.
XX
XX ADS28058;
XX
XX 02-DEC-2004 (first entry)
XX
XX Bacterial polypeptide #17091.
XX
XX Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
XX Bacteria.
XX
XX US2003233675-A1.
XX
XX 18-DEC-2003.
XX
XX 20-FEB-2003; 2003US-00369493.
XX
XX 21-FEB-2002; 2002US-0360039P.
XX
XX (CAOY/) CAO Y.
XX (HINK/) HINKLE G J.
XX (SLAT/) SLATER S C.
XX (CHEN/) CHEN X.
XX (GOLD/) GOLDMAN B S.
XX
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX
XX WPI; 2004-061375/06.
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
XX for expression of a polynucleotide encoding a polypeptide from a
XX microbial source, useful for producing plants with improved properties.
XX
XX Claim 1; SEQ ID NO 17091; 122pp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a
XX promoter functional in a plant cell, where the promoter is positioned to
XX provide for expression of a polynucleotide encoding a polypeptide from a
XX microbial source. The invention also relates to a transformed plant
XX comprising the recombinant DNA construct and a method of producing a
XX transformed plant having an improved property. The plant is a crop plant
XX such as maize or soybean. The method of producing a transformed plant
XX having an improved property comprises transforming a plant with the
XX recombinant DNA construct and growing the transformed plant, where the
XX polynucleotide or polypeptide is useful for improving plant properties.
XX The recombinant DNA construct is useful for producing plants with
XX improved plant properties, e.g. improved cold heat or drought tolerance,
XX tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
XX increased resistance to plant disease, better growth rate by modification
XX of the cell cycle pathway with plant growth regulators, increased rate of
XX homologous recombination, modified seed oil or protein yield and/or
XX content, improved yield by modification of carbohydrate, nitrogen or
XX phosphorus use and/or uptake, by modification of photosynthesis or by
XX providing improved plant growth and development under at least one stress
XX condition, improved lignin production or improved galactomannan
XX production. This sequence represents a bacterial polypeptide used in the
XX scope of the invention. Note: The sequence data for this patent did not
XX form part of the printed specification but was obtained in electronic
XX format from USPTO at seqdata.uspto.gov/sequence.html.
XX
XX Sequence 231 AA;
SQ
Query Match      68.0%; Score 34; DB 8; Length 231;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASTIAARVLD 10
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Db |:||||| 100 ATTAARKLD 109

RESULT 14
AAG20306
ID AAG20306 standard; protein, 237 AA.
XX
AC AAG20306;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 22440.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
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PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
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PR 19-APR-1999; 99US-0130077P.
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PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
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PR 30-APR-1999; 99US-0132048P.
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PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
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PR 22-JUN-1999; 99US-0139899P.
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PR 12-AUG-1999; 99US-0148341P.
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PR	20-AUG-1999;	99US-0149723P.	XX	XX	Protein identification; signal transduction pathway; metabolic pathway;
PR	20-AUG-1999;	99US-0149929P.	XX	XX	hybridisation assay; genetic mapping; gene expression control; promoter;
PR	20-AUG-1999;	99US-0149902P.	XX	XX	termination sequence.
PR	23-AUG-1999;	99US-0149930P.	DE	DE	Arabidopsis thaliana.
PR	26-AUG-1999;	99US-0150566P.	KW	KW	Arabidopsis thaliana.
PR	26-AUG-1999;	99US-0150884P.	KW	KW	EP1033405-A2.
PR	27-AUG-1999;	99US-0151065P.	KW	KW	06-SEP-2000.
PR	27-AUG-1999;	99US-0151066P.	XX	XX	25-FEB-2000; 2000EP-00301439.
PR	27-AUG-1999;	99US-0151080P.	XX	XX	25-FEB-1999; 99US-0121825P.
PR	30-AUG-1999;	99US-0151303P.	XX	XX	05-MAR-1999; 99US-0123180P.
PR	31-AUG-1999;	99US-0151308P.	PN	PN	09-MAR-1999; 99US-0123548P.
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PR	07-SEP-1999;	99US-0152363P.	XX	XX	25-MAR-1999; 99US-0126264P.
PR	10-SEP-1999;	99US-0153070P.	XX	XX	29-MAR-1999; 99US-0126785P.
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PR	15-SEP-1999;	99US-0154018P.	XX	XX	06-APR-1999; 99US-0128234P.
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PR	23-SEP-1999;	99US-0155486P.	XX	XX	21-APR-1999; 99US-0130449P.
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PR	21-OCT-1999;	99US-0160814P.	XX	XX	01-JUN-1999; 99US-0137222P.
PR	21-OCT-1999;	99US-0160815P.	XX	XX	03-JUN-1999; 99US-0137528P.
PR	22-OCT-1999;	99US-0160981P.	XX	XX	04-JUN-1999; 99US-0137502P.
PR	22-OCT-1999;	99US-0160981P.	XX	XX	07-JUN-1999; 99US-0137724P.
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PR	26-OCT-1999;	99US-0161360P.	XX	XX	16-JUN-1999; 99US-0139453P.
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PR	28-OCT-1999;	99US-0161920P.	XX	XX	18-JUN-1999; 99US-0139456P.
PR	28-OCT-1999;	99US-0161920P.	XX	XX	18-JUN-1999; 99US-0139457P.
PR	28-OCT-1999;	99US-0161920P.	XX	XX	18-JUN-1999; 99US-0139458P.
PR	28-OCT-1999;	99US-0161920P.	XX	XX	18-JUN-1999; 99US-0139459P.
PR	28-OCT-1999;	99US-0161920P.	XX	XX	18-JUN-1999; 99US-0139460P.
PR	28-OCT-1999;	99US-0161920P.	XX	XX	18-JUN-1999; 99US-0139461P.

Query Match 68.0%; Score 34; DB 3; Length 237;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AARVLDY 11
Db 8 AARVLDY 14

RESULT 15
AAG51887
ID AAG51887 standard; protein; 237 AA.

PR 18-JUN-1999;	99US-0139462P.	PR 25-AUG-1999;	99US-0150566P.
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PR 21-JUL-1999;	99US-0145086P.	PR 21-OCT-1999;	99US-0160767P.
PR 21-JUL-1999;	99US-0145088P.	PR 21-OCT-1999;	99US-0160768P.
PR 22-JUL-1999;	99US-0145085P.	PR 21-OCT-1999;	99US-0160770P.
PR 22-JUL-1999;	99US-0145087P.	PR 21-OCT-1999;	99US-0160814P.
PR 22-JUL-1999;	99US-0145089P.	PR 21-OCT-1999;	99US-0160815P.
PR 22-JUL-1999;	99US-0145192P.	PR 22-OCT-1999;	99US-0160815P.
PR 23-JUL-1999;	99US-0145145P.	PR 22-OCT-1999;	99US-0160980P.
PR 23-JUL-1999;	99US-0145218P.	PR 22-OCT-1999;	99US-0160981P.
PR 23-JUL-1999;	99US-0145224P.	PR 25-OCT-1999;	99US-0161404P.
PR 26-JUL-1999;	99US-0145276P.	PR 25-OCT-1999;	99US-0161405P.
PR 27-JUL-1999;	99US-0145913P.	PR 26-OCT-1999;	99US-0161406P.
PR 27-JUL-1999;	99US-0145918P.	PR 26-OCT-1999;	99US-0161359P.
PR 27-JUL-1999;	99US-0145919P.	PR 26-OCT-1999;	99US-0161360P.
PR 28-JUL-1999;	99US-0145951P.	PR 26-OCT-1999;	99US-0161361P.
PR 02-AUG-1999;	99US-0146386P.	PR 28-OCT-1999;	99US-0161920P.
PR 02-AUG-1999;	99US-0146388P.	PR 28-OCT-1999;	99US-0161922P.
PR 02-AUG-1999;	99US-0146389P.	PR 28-OCT-1999;	99US-0161933P.
PR 03-AUG-1999;	99US-0147038P.	PR 29-OCT-1999;	99US-0162142P.
PR 04-AUG-1999;	99US-0147204P.		
PR 04-AUG-1999;	99US-0147302P.		
PR 05-AUG-1999;	99US-0147192P.		
PR 05-AUG-1999;	99US-0147260P.		
PR 06-AUG-1999;	99US-0147303P.		
PR 06-AUG-1999;	99US-0147303P.		
PR 09-AUG-1999;	99US-0147416P.		
PR 09-AUG-1999;	99US-0147493P.		
PR 09-AUG-1999;	99US-0147935P.		
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PR 12-AUG-1999;	99US-0148341P.		
PR 13-AUG-1999;	99US-0148565P.		
PR 13-AUG-1999;	99US-0148684P.		
PR 16-AUG-1999;	99US-0149368P.		
PR 17-AUG-1999;	99US-0149175P.		
PR 18-AUG-1999;	99US-0149426P.		
PR 20-AUG-1999;	99US-0149722P.		
PR 20-AUG-1999;	99US-0149723P.		
PR 20-AUG-1999;	99US-0149929P.		
PR 23-AUG-1999;	99US-0149902P.		
PR 23-AUG-1999;	99US-0149930P.		

Query Match 68.0%; Score 34; DB 3; Length 237;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AARVLDY 11
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DB 8 AARVLDY 14

Search completed: October 14, 2005, 16:12:40
Job time : 85.5625 secs

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OM protein - protein search, using sw model

Run on: October 14, 2005, 16:00:04 ; Search time 21.6562 Seconds
(without alignments)
37.917 Million cell updates/sec

Title: US-10-614-959-12
Perfect score: 50
Sequence: 1 ASIAAARVLDY 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	46	92.0	11	4	US-09-383-667-19	Sequence 19, Appl
3	36	72.0	755	3	US-09-342-648-2	Sequence 2, Appl
4	34	68.0	278	2	US-08-865-203-6	Sequence 6, Appl
5	34	68.0	278	2	US-07-849-420-6	Sequence 6, Appl
6	34	68.0	278	3	US-09-253-854-6	Sequence 6, Appl
7	34	68.0	278	3	US-08-955-424-6	Sequence 6, Appl
8	34	68.0	279	2	US-09-133-658-4	Sequence 6, Appl
9	34	68.0	279	4	US-09-512-251A-6	Sequence 6, Appl
10	34	68.0	279	4	US-09-515-150A-6	Sequence 6, Appl
11	34	68.0	279	4	US-09-196-281-9	Sequence 9, Appl
12	34	68.0	279	6	5472855-6	Patent No. 5472855
13	34	68.0	279	6	5472855-6	Patent No. 5472855
14	33	66.0	85	4	US-09-698-286A-10	Sequence 10, Appl
15	33	66.0	194	4	US-09-710-279-622	Sequence 622, App
16	33	66.0	223	3	US-09-134-001C-3417	Sequence 3417, Ap
17	33	66.0	331	4	US-09-248-796A-18164	Sequence 18164, A
18	33	66.0	364	4	US-09-489-039A-12051	Sequence 12051, A
19	33	66.0	402	4	US-09-602-787A-508	Sequence 508, App
20	33	66.0	867	4	US-09-540-236-3193	Sequence 3193, Ap
21	33	66.0	910	4	US-09-902-540-16309	Sequence 16309, A
22	32	64.0	234	4	US-09-252-991A-17003	Sequence 17003, A
23	32	64.0	280	4	US-09-724-797-34	Sequence 34, Appl
24	32	64.0	480	4	US-09-252-991A-31470	Sequence 31470, A
25	31	62.0	111	4	US-09-902-540-10906	Sequence 10906, A
26	31	62.0	177	3	US-08-975-762-38	Sequence 38, Appl
27	31	62.0	177	3	US-08-975-762-55	Sequence 55, Appl

ALIGNMENTS

RESULT 1

US-09-383-667-12
; Sequence 12, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camelia W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Eaton, Dan L.
; APPLICANT: Hass, Philip E.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Kirchofer, Daniel
; APPLICANT: Suggett, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: P1661R2
; CURRENT APPLICATION NUMBER: US/09/383,667
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,233
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: US 60/122,767
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 12
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-667-12

Query Match 100.0%; Score 50; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ASIAAARVLDY 11

RESULT 2

US-09-383-667-19
; Sequence 19, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camelia W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Eaton, Dan L.
; APPLICANT: Hass, Philip E.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Kirchofer, Daniel
; APPLICANT: Suggett, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: P1661R2

; CURRENT APPLICATION NUMBER: US/09/383.667
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098.233
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: US 60/122.767
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 19
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-667-19

Query Match 92.0%; Score 46; DB 4; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0013;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ASIAAARVLDY 11
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Db 1 ASIAAGRVLDY 11

RESULT 3
US-09-342-648-2
; Sequence 2, Application US/09342648
; Patent No. 6248584
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Odell, Joan
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: Transcription Coactivators
; FILE REFERENCE: BB-1169-B
; CURRENT APPLICATION NUMBER: US/09/342.648
; CURRENT FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: 60/092.659
; EARLIER FILING DATE: July 13, 1998
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 2
; LENGTH: 755
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (179)
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (185)
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (241)
US-09-342-648-2

Query Match 72.0%; Score 36; DB 3; Length 755;
Best Local Similarity 72.7%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ASIAAARVLDY 11
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Db 240 AXIADTRVLDY 250

RESULT 4
US-08-865-203-6
; Sequence 6, Application US/08865203
; Patent No. 5935815
; GENERAL INFORMATION:
; APPLICANT: van de Ven, Willem Jan Marie
; APPLICANT: van den Ouweland, Anna Maria Wilhelmina
; APPLICANT: Van Duijnhooven, Johannes Lambertus Petrus
; APPLICANT: Robroek, Antonius Johannes Maria
; APPLICANT: Koning, Piet Nico Maria
; TITLE OF INVENTION: Pharmaceutical Composition Having An

; TITLE OF INVENTION: Endoproteolytic Activity; A Process for
; TITLE OF INVENTION: Endoproteolytically Processing (Precursor)
; TITLE OF INVENTION: Proteins And For The (Micro)Biological
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOFFMANN & BARON, LLP
; STREET: 350 Jericho Turnpike
; CITY: Jericho
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11753
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/865.203
; FILING DATE: 29-MAY-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Tran, Jessica H.
; REGISTRATION NUMBER: 40,846
; REFERENCE/DOCKET NUMBER: 294-41 DIV II
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 822-3550
; TELEFAX: (516) 822-3582
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 278 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-865-203-6

Query Match 68.0%; Score 34; DB 2; Length 278;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASIAAARVLD 10
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Db 96 ASILAVRVLD 105

RESULT 5
US-07-849-420-6
; Sequence 6, Application US/07849420
; Patent No. 5989856
; GENERAL INFORMATION:
; APPLICANT: van de Ven, Willem Jan Marie
; APPLICANT: van den Ouweland, Anna Maria Wilhelmina
; APPLICANT: Van Duijnhooven, Johannes Lambertus Petrus
; APPLICANT: Robroek, Antonius Johannes Maria
; APPLICANT: Koning, Piet Nico Maria
; TITLE OF INVENTION: Pharmaceutical Composition Having An
; TITLE OF INVENTION: Endoproteolytic Activity; A Process for
; TITLE OF INVENTION: Endoproteolytically Processing (Precursor)
; TITLE OF INVENTION: Proteins And For The (Micro)Biological
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICANT: US/07/849,420
FILING DATE: 19920624
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Moran, Thomas F.
REGISTRATION NUMBER: 16,579
REFERENCE/DOCKET NUMBER: 2805/41413
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 977-9550
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 278 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-849-420-6

Query Match 68.0%; Score 34; DB 2; Length 278;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ASIAARVLD 10
Db 96 ASILAVRVD 105

RESULT 6
US-09-253-854-6
Sequence 6, Application US/09253854
Patent No. 6132717
GENERAL INFORMATION:
APPLICANT: van de Ven, Willem Jan Marie;
APPLICANT: van den Ouweland, Anna Maria Wilhelmina;
APPLICANT: Van Duijnhoven, Johannes Lambertus Petrus;
APPLICANT: Robroek, Antonius Johannes Maria; and
APPLICANT: Koning, Piet Nico Maria
TITLE OF INVENTION: Pharmaceutical Composition Having An
TITLE OF INVENTION: Endoproteolytic Activity; A Process for
TITLE OF INVENTION: Endoproteolytically Processing (Precursor)
TITLE OF INVENTION: Proteins And For The (Micro)Biological
TITLE OF INVENTION: Production Of Proteins
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOFFMANN & BARON, LLP
STREET: 350 Jericho Turnpike
CITY: Jericho
STATE: New York
COUNTRY: U.S.A.
ZIP: 11753
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/253,854
FILING DATE: Unassigned

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Tran, Jessica H.
REGISTRATION NUMBER: 40,846
REFERENCE/DOCKET NUMBER: 294-41 DIV II/CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 822-3550
TELEFAX: (516) 822-3582
TELEX:
INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 278 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-253-854-6
Query Match 68.0%; Score 34; DB 3; Length 278;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ASIAARVLD 10
Db 96 ASILAVRVD 105

RESULT 7
US-08-955-424-6
Sequence 6, Application US/08955424
Patent No. 6274365
GENERAL INFORMATION:
APPLICANT: Van de Ven, Willem Jan Marie
APPLICANT: Van den Ouweland, Anna Maria Wilhelmina
APPLICANT: Van Duijnhoven, Johannes Lambertus Petrus
APPLICANT: Koning, Piet Nico Maria
APPLICANT: Robroek, Antonius Johannes Maria
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION HAVING AN ENDOPEPTOLYTIC
TITLE OF INVENTION: ACTIVITY: A PROCESS FOR ENDOPEPTOLYTICALLY PROCESSING
TITLE OF INVENTION: (PRECURSOR) PROTEINS AND FOR THE (MICRO) BIOLOGICAL
TITLE OF INVENTION: PRODUCTION OF PROTEINS
FILE REFERENCE: SEQUENCE LISTINGS 1-12 294-41 DIV/FWC
CURRENT APPLICATION NUMBER: US/08/955,424
CURRENT FILING DATE: 1997-10-22
EARLIER APPLICATION NUMBER: 08/568,152
EARLIER FILING DATE: 1995-06-12
EARLIER APPLICATION NUMBER: 07/849,420
EARLIER FILING DATE: 1992-06-24
EARLIER APPLICATION NUMBER: PCT/NL90/00151
EARLIER FILING DATE: 1990-10-21
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 278
TYPE: PRT
ORGANISM: Thermoactinomyces vulgaris
US-08-955-424-6

Query Match 68.0%; Score 34; DB 3; Length 278;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ASIAARVLD 10
Db 96 ASILAVRVD 105

RESULT 8
US-09-135-658-4
Sequence 4, Application US/09135658
Patent No. 5972683
GENERAL INFORMATION:
APPLICANT: TSAI, Ying-Chieh
TITLE OF INVENTION: MUTANT TYPE SUBTILISIN YAB AND ITS APPLICATION
FILE REFERENCE: 6653-011-999
CURRENT APPLICATION NUMBER: US/09/135,658
CURRENT FILING DATE: 1998-08-18
EARLIER APPLICATION NUMBER: 86112766
EARLIER FILING DATE: 1997-09-04
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0 - beta
SEQ ID NO 4
LENGTH: 279

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; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-09-135-658-4

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Best Local Similarity 80.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 0; Indels 2; Gaps 0;

Qy 1 ASIAAARVLD 10
Db 96 ASILAVRVLD 105

RESULT 9
US-09-512-251A-6
; Sequence 6, Application US/09512251A
; Patent No. 6555355
; GENERAL INFORMATION:
; APPLICANT: Hansen, Peter
; APPLICANT: Bauditz, Peter
; APPLICANT: Mikkelsen, Frank
; APPLICANT: Andersen, Kim
; TITLE OF INVENTION: Protease Variants and Compositions
; FILE REFERENCE: 5349.204-US
; CURRENT APPLICATION NUMBER: US/09/512.251A
; CURRENT FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Bacillus
US-09-512-251A-6

Query Match      68.0%; Score 34; DB 4; Length 279;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 0; Indels 2; Gaps 0;

Qy 1 ASIAAARVLD 10
Db 96 ASILAVRVLD 105

RESULT 10
US-09-515-150A-6
; Sequence 6, Application US/09515150A
; Patent No. 6558938
; GENERAL INFORMATION:
; APPLICANT: Hansen, Peter
; APPLICANT: Bauditz, Peter
; APPLICANT: Mikkelsen, Frank
; APPLICANT: Andersen, Kim
; TITLE OF INVENTION: Protease Variants and Compositions
; FILE REFERENCE: 5348.204-US
; CURRENT APPLICATION NUMBER: US/09/515.150A
; CURRENT FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Bacillus
US-09-515-150A-6

Query Match      68.0%; Score 34; DB 4; Length 279;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 0; Indels 2; Gaps 0;

Qy 1 ASIAAARVLD 10
Db 96 ASILAVRVLD 105

RESULT 11
US-09-196-281-9
; Sequence 9, Application US/09196281A
; Patent No. 6605458
; GENERAL INFORMATION:
; APPLICANT: Hansen, Peter K.
; APPLICANT: Bauditz, Peter
; APPLICANT: Mikkelsen, Frank
; TITLE OF INVENTION: Protease Variants And Compositions
; FILE REFERENCE: 5435.200-US
; CURRENT APPLICATION NUMBER: US/09/196.281A
; CURRENT FILING DATE: 1998-11-19
; EARLIER APPLICATION NUMBER: 1332/97
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Bacillus
US-09-196-281-9

Query Match      68.0%; Score 34; DB 4; Length 279;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASIAAARVLD 10
Db 96 ASILAVRVLD 105

RESULT 12
5472855-6
; Patent No. 5472855
; APPLICANT: CARTER, PAUL J.; WELLS, JAMES A.
; TITLE OF INVENTION: SUBSTRATE ASSISTED CATALYSIS
; NUMBER OF SEQUENCES: 31
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/287,964
; FILING DATE: 22-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 90,902
; FILING DATE: 12-JUL-1993
; APPLICATION NUMBER: 823,039
; FILING DATE: 14-JAN-1992
; APPLICATION NUMBER: 35,652
; FILING DATE: 06-APR-1987
; APPLICATION NUMBER: 334,081
; FILING DATE: 04-APR-1989
; APPLICATION NUMBER: 127,134
; FILING DATE: 01-DEC-1987
; APPLICATION NUMBER: 846,627
; FILING DATE: 01-APR-1986
; APPLICATION NUMBER: 858,594
; FILING DATE: 30-APR-1986
; APPLICATION NUMBER: 614,612
; FILING DATE: 29-MAY-1984
; APPLICATION NUMBER: 614,615
; FILING DATE: 29-MAY-1984
; APPLICATION NUMBER: 614,617
; FILING DATE: 29-MAY-1984
; APPLICATION NUMBER: 614,491
; FILING DATE: 29-MAY-1984
; SEQ ID NO:6;
; LENGTH: 279
5472855-6

Query Match      68.0%; Score 34; DB 6; Length 279;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASIAAARVLD 10
Db 96 ASILAVRVLD 105
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; NAME/KEY: MISC_FEATURE
; LOCATION: (30)..(33)
; OTHER INFORMATION: Gap in alignment
US-09-698-286A-10

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Best Local Similarity 70.0%; Pred. No. 9.8;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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DB      71 SIAAGKPLDY 80

RESULT 15
US-09-710-279-622
; Sequence 622, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 622
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-09-710-279-622

Query Match      66.0%; Score 33; DB 4; Length 194;
Best Local Similarity 60.0%; Pred. No. 26;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      2 SIAAARVLDY 11
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DB      106 NVASASVLDY 115
  
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Search completed: October 14, 2005, 16:22:01
Job time : 22.6562 secs

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; DB      96 ASILAVRVLD 105

RESULT 13
5472855-6
; Patent No. 5472855
; APPLICANT: CARTER, PAUL J.; WELLS, JAMES A.
; TITLE OF INVENTION: SUBSTRATE ASSISTED CATALYSIS
; NUMBER OF SEQUENCES: 31
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/287,964
; FILING DATE: 22-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 90,902
; FILING DATE: 12-JUL-1993
; APPLICATION NUMBER: 823,039
; FILING DATE: 14-JAN-1992
; APPLICATION NUMBER: 35,652
; FILING DATE: 06-APR-1987
; APPLICATION NUMBER: 334,081
; FILING DATE: 04-APR-1989
; APPLICATION NUMBER: 127,134
; FILING DATE: 01-DEC-1987
; APPLICATION NUMBER: 846,627
; FILING DATE: 01-APR-1986
; APPLICATION NUMBER: 858,594
; FILING DATE: 30-APR-1986
; APPLICATION NUMBER: 614,612
; FILING DATE: 29-MAY-1984
; APPLICATION NUMBER: 614,615
; FILING DATE: 29-MAY-1984
; APPLICATION NUMBER: 614,617
; FILING DATE: 29-MAY-1984
; APPLICATION NUMBER: 614,491
; FILING DATE: 29-MAY-1984
; SEQ ID NO: 6
; LENGTH: 279
5472855-6

Query Match      68.0%; Score 34; DB 6; Length 279;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 ASIAAARVLD 10
      |||||:||||
DB      96 ASILAVRVLD 105

RESULT 14
US-09-698-286A-10
; Sequence 10, Application US/09698286A
; Patent No. 6677442
; GENERAL INFORMATION:
; APPLICANT: University of Kentucky Research Foundation
; TITLE OF INVENTION: Human REV1 Gene and Protein As Diagnostic, Preventive, and Therap
; FILE REFERENCE: 050229-0247
; CURRENT APPLICATION NUMBER: US/09/698,286A
; CURRENT FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 60/162,140
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 85
; TYPE: PRT
; ORGANISM: C. elegans, A. thaliana, S. cerevisiae, S. pombe and H. sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (17)..(22)
; OTHER INFORMATION: Gap in alignment
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (50)..(60)
  
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2005, 16:20:10 ; Search time 78.2031 Seconds
(without alignments)
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Title: US-10-614-959-12
Perfect score: 50
Sequence: 1 ASIAARVLDY 11

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Searched: 1859788 seqs, 41671961 residues

Total number of hits satisfying chosen parameters: 1859788

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	40	80.0	183	US-10-425-115-369042	Sequence 369042,
2	37	74.0	408	US-10-389-566-831	Sequence 831, App
3	37	74.0	573	US-10-425-114-45344	Sequence 45544, A
4	37	74.0	573	US-10-425-115-208229	Sequence 208229,
5	37	74.0	694	US-10-425-115-208239	Sequence 208239,
6	37	74.0	1203	US-10-437-963-120758	Sequence 120758,
7	36	72.0	652	US-10-369-493-14688	Sequence 14688, A
8	36	72.0	652	US-10-369-493-15165	Sequence 15165, A
9	36	72.0	655	US-10-369-493-14406	Sequence 14406, A
10	36	72.0	656	US-10-369-493-11635	Sequence 11635, A
11	36	72.0	1064	US-10-437-963-189048	Sequence 189048,

12	35	70.0	45	16	US-10-437-963-201347	Sequence 201347,
13	35	70.0	107	16	US-10-437-963-175236	Sequence 175236,
14	34	68.0	198	16	US-10-767-701-38892	Sequence 38892, A
15	34	68.0	231	15	US-10-369-493-17091	Sequence 17091, A
16	34	68.0	279	14	US-10-336-324-6	Sequence 6, Appl
17	34	68.0	279	14	US-10-403-105-9	Sequence 9, Appl
18	34	68.0	341	16	US-10-425-115-353435	Sequence 353435,
19	34	68.0	642	16	US-10-767-701-45651	Sequence 45651, A
20	34	68.0	671	15	US-10-369-493-7093	Sequence 7093, Ap
21	34	68.0	674	15	US-10-369-493-4338	Sequence 4338, Ap
22	34	68.0	691	15	US-10-425-114-70274	Sequence 70274, A
23	34	68.0	827	16	US-10-437-963-146706	Sequence 146706,
24	34	68.0	1000	16	US-10-437-963-122779	Sequence 122779,
25	33	66.0	204	14	US-10-238-075-276	Sequence 276, App
26	33	66.0	223	18	US-10-724-972A-5583	Sequence 5583, App
27	33	66.0	274	14	US-10-032-585-7697	Sequence 7697, Ap
28	33	66.0	299	15	US-10-425-114-40808	Sequence 40808, A
29	33	66.0	331	14	US-10-156-761-8701	Sequence 8701, Ap
30	33	66.0	358	15	US-10-282-122A-62045	Sequence 62045, A
31	33	66.0	358	15	US-10-282-122A-63923	Sequence 63923, A
32	33	66.0	367	15	US-10-282-122A-62857	Sequence 62857, A
33	33	66.0	367	15	US-10-282-122A-64830	Sequence 64830, A
34	33	66.0	371	20	US-11-058-046-5	Sequence 5, Appl
35	33	66.0	402	15	US-10-627-476-508	Sequence 508, App
36	33	66.0	449	9	US-09-738-626-6555	Sequence 6555, Ap
37	33	66.0	453	15	US-10-369-493-21054	Sequence 21054, A
38	33	66.0	466	16	US-10-437-963-136788	Sequence 136788,
39	33	66.0	469	15	US-10-417-700A-49	Sequence 49, Appl
40	33	66.0	509	15	US-10-282-122A-77407	Sequence 77407, A
41	33	66.0	670	15	US-10-369-493-11847	Sequence 11847, A
42	33	66.0	862	16	US-10-425-115-189243	Sequence 189243,
43	33	66.0	867	15	US-10-282-122A-63141	Sequence 63141, A
44	33	66.0	1958	14	US-10-152-886-53	Sequence 53, Appl
45	33	66.0	1958	20	US-11-053-576-53	Sequence 53, Appl

ALIGNMENTS

RESULT 1

US-10-425-115-369042
; Sequence 369042, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 369042
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(183)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_99740C.1.pep
US-10-425-115-369042

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Best Local Similarity 90.0%; Pred. No. 7.9;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY . 2 SIAAARVLDY 11

Db 91 SIAADRVDY 100

RESULT 4
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; Sequence 208229, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT FILING DATE: 2003-04-28
; CURRENT APPLICATION NUMBER: US/10/425,115
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 208229
; LENGTH: 573
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_121499C.1.pep
US-10-425-115-208229
Query Match 74.0%; Score 37; DB 16; Length 573;
Best Local Similarity 72.7%; Pred. No. 1e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ASIAAARVLDY 11
Db 58 ANIADTRVLDY 68
RESULT 5
US-10-425-115-208239
; Sequence 208239, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT FILING DATE: 2003-04-28
; CURRENT APPLICATION NUMBER: US/10/425,115
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 208239
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_121507C.1.pep
US-10-425-115-208239
Query Match 74.0%; Score 37; DB 16; Length 694;
Best Local Similarity 72.7%; Pred. No. 1.3e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ASIAAARVLDY 11
Db 179 ANIADTRVLDY 189
RESULT 6
US-10-437-963-120758
; Sequence 120758, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua

US-10-389-566-831
; Sequence 831, Application US/10389566
; Publication No. US20040025202A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)D
; CURRENT FILING DATE: 2003-03-31
; CURRENT APPLICATION NUMBER: US/10/389,566
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2459
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 831
; LENGTH: 408
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (103)..(104)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-389-566-831
Query Match 74.0%; Score 37; DB 15; Length 408;
Best Local Similarity 80.0%; Pred. No. 73;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 ASIAAARVLD 10
Db 275 ASLAARALD 284
RESULT 3
US-10-425-114-45544
; Sequence 45544, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53313)B
; CURRENT FILING DATE: 2003-04-28
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 45544
; LENGTH: 573
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700800359_FLI.pep
US-10-425-114-45544
Query Match 74.0%; Score 37; DB 15; Length 573;
Best Local Similarity 72.7%; Pred. No. 1e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ASIAAARVLDY 11
Db 58 ANIADTRVLDY 68

APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 120758
LENGTH: 1203
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT MRT4530_2384C.1.pep
US-10-437-963-120758

Query Match 74.0%; Score 37; DB 16; Length 1203;
Best Local Similarity 70.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASIAAARVLD 10
Db 330 ASVAATRIID 339

RESULT 7
US-10-369-493-14688
; Sequence 14688, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 14688
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-14688

Query Match 72.0%; Score 36; DB 15; Length 652;
Best Local Similarity 63.6%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAAARVLDY 11
Db 255 AATAAARAIDY 265

RESULT 8
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; Sequence 15165, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 11635

FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 15165
LENGTH: 652
TYPE: PRT
ORGANISM: Agrobacterium tumefaciens
US-10-369-493-15165

Query Match 72.0%; Score 36; DB 15; Length 652;
Best Local Similarity 63.6%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAAARVLDY 11
Db 255 AATAAARAIDY 265

RESULT 9
US-10-369-493-14406
; Sequence 14406, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 14406
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-14406

Query Match 72.0%; Score 36; DB 15; Length 655;
Best Local Similarity 63.6%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAAARVLDY 11
Db 255 AATAAARAIDY 265

RESULT 10
US-10-369-493-11635
; Sequence 11635, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 11635

FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_96731C.1.pep
US-10-437-963-201347

Query Match 70.0%; Score 35; DB 16; Length 45;
Best Local Similarity 88.9%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 STAAARVLD 10
|:|||||
DB 16 SIATARVLD 24

RESULT 13

US-10-437-963-175236
; Sequence 175236, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 175236
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(107)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_73100C.1.pep
US-10-437-963-175236

Query Match 70.0%; Score 35; DB 16; Length 107;
Best Local Similarity 80.0%; Pred. No. 45;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASIAAARVLD 10
|:|||||
DB 34 ASLAARVSD 43

RESULT 14

US-10-767-701-38892
; Sequence 38892, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 38892
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C77436_1.pep

LENGTH: 656
TYPE: PRT
ORGANISM: Agrobacterium tumefaciens
US-10-369-493-11635

Query Match 72.0%; Score 36; DB 15; Length 656;
Best Local Similarity 63.6%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAAARVLDY 11
|:|||||
DB 255 AATAAARAIDY 265

RESULT 11

US-10-437-963-189048
; Sequence 189048, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 189048
; LENGTH: 1064
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_85594C.1.pep
US-10-437-963-189048

Query Match 72.0%; Score 36; DB 16; Length 1064;
Best Local Similarity 80.0%; Pred. No. 3.2e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASIAAARVLD 10
|:|||||
DB 116 ASLAARVLD 125

RESULT 12

US-10-437-963-201347
; Sequence 201347, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 201347
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Oryza sativa

✓US-10-767-701-38892

Query Match 68.0%; Score 34; DB 16; Length 198;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AARVLDY 11
|:|||||
Db 114 AARVLDY 120

RESULT 15

US-10-369-493-17091
; Sequence 17091, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 17091
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Caulobacter crescentus
US-10-369-493-17091

Query Match 68.0%; Score 34; DB 15; Length 231;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASIAAARVLD 10
|:|||||
Db 100 ATIAAARKLD 109

Search completed: October 14, 2005, 17:00:43
Job time : 79.2031 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2005, 16:02:59 ; Search time 15.2969 Seconds
(without alignments)
69.190 Million cell updates/sec

Title: US-10-614-959-12
Perfect score: 50
Sequence: 1 ASIAAARVLDY 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	36	72.0	663	2	AF2984	3-methylcrotonyl-C
2	36	72.0	709	2	A98299	3-methylcrotonyl-C
3	35	70.0	143	2	S43071	hypothetical prote
4	35	70.0	692	2	S56849	probable membrane
5	35	70.0	696	2	AB1210	teichoic acid bios
6	34	68.0	231	2	D87715	carboxymethylenebu
7	34	68.0	279	1	SUMITV	thermitase (EC 3.4
8	34	68.0	579	2	I40371	methyltransferase
9	34	68.0	649	2	T38883	hypothetical prote
10	34	68.0	956	2	B71468	probable insulinas
11	33	66.0	162	2	AF1059	probable transcrip
12	33	66.0	202	2	AF2831	DNA polymerase III
13	33	66.0	202	2	B97609	probable DNA polym
14	33	66.0	220	2	F89878	conserved hypothet
15	33	66.0	264	2	G69213	hypothetical prote
16	33	66.0	358	2	T45400	hypothetical prote
17	33	66.0	367	2	C70858	hypothetical prote
18	33	66.0	397	2	C84904	hypothetical prote
19	33	66.0	441	2	A75619	hypothetical prote
20	33	66.0	482	2	H70463	cobyrinic acid a,c
21	33	66.0	509	2	G82104	glutamine dehydrog
22	33	66.0	614	2	S45053	glutamyl-tRNA synt
23	33	66.0	1027	2	T27970	membrane protein E
24	33	66.0	1232	2	T06165	hypothetical prote
25	32	64.0	305	2	E85437	multidrug resistanc
26	32	64.0	342	2	G69502	histidinyl aminopep
27	32	64.0	363	2	D64640	histidinol-phospha
28	32	64.0	365	2	C87712	hypothetical prote
29	32	64.0	409	2	AG2869	carbohydrate kinas
						N-carbamoyl-beta-a

30	32	64.0	415	2	A97646	n-carbamoyl-beta-a
31	32	64.0	435	2	T20819	hypothetical prote
32	32	64.0	448	2	T16256	hypothetical prote
33	32	64.0	576	1	B70558	probable ABC trans
34	32	64.0	655	2	G96524	protein T1N15.9 [1
35	32	64.0	777	2	G95940	probable xanthine
36	32	64.0	817	2	T45642	hypothetical prote
37	31	62.0	119	2	T16347	hypothetical prote
38	31	62.0	131	2	AG2388	hypothetical prote
39	31	62.0	144	2	C75376	hypothetical prote
40	31	62.0	172	2	S75615	hypothetical prote
41	31	62.0	177	2	B83036	hypothetical prote
42	31	62.0	230	2	AF3541	probable bacteriof
43	31	62.0	249	2	A81001	glutathione transfer
44	31	62.0	249	2	F82018	electron transfer
45	31	62.0	254	2	AC3018	conserved hypothet

ALIGNMENTS

RESULT 1
AF2984
3-methylcrotonyl-CoA carboxylase alpha subunit [imported] - Agrobacterium tumefaciens (s
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AF2984
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, J
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AF2984
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-663 <KUR>
A:CROSS-references: UNIPROT:Q8UA95; GB:AE008689; PIDN:AA44292.1; PID:g17741880; GSPDB:G
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: mcca
A:Map position: linear chromosome
C:Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; lipoy

Query Match 72.0%; Score 36; DB 2; Length 663;
Best Local Similarity 63.6%; Pred. No. 27;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAAARVLDY 11
|:||||:|
Db 258 AATAAARAIDY 268

RESULT 2
A98299
3-methylcrotonyl-CoA carboxylase alpha chain (AF310338) [imported] - Agrobacterium tumef
C:Species: Agrobacterium tumefaciens
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: A98299
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: A98299
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-709 <KUR>
A:CROSS-references: UNIPROT:Q8UA95; GB:AE007870; PIDN:AAK89915.1; PID:g15159866; GSPDB:G
C:Genetics:
A:Gene: AGR_L_2704

A;Map position: linear chromosome
C;Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; lipoyl

Query Match 72.0%; Score 36; DB 2; Length 709;
Best Local Similarity 63.6%; Pred. No. 29;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTAAARVLDY 11
|:|||||:
Db 304 AATAAARAIDY 314

RESULT 3
S43071
hypotheical protein 5 - human herpesvirus 6
C;Species: human herpesvirus 6
C;Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C;Accession: S43071
R;Thompson, J.; Choudhury, S.; Kashanchi, F.; Doniger, J.; Berneman, Z.; Frenkel, N.; R
Oncogene 9, 1167-1175, 1994
A;Title: A transforming fragment within the direct repeat region of human herpesvirus ty
A;Reference number: S43067; MUID:94181269; PMID:8134119
A;Accession: S43071
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-143 <THO>
A;Cross-references: UNIPROT:Q69582; EMBL:X73675; NID:9469952; PIDN:CAA52028.1; PID:94699
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1993

Query Match 70.0%; Score 35; DB 2; Length 143;
Best Local Similarity 88.9%; Pred. No. 8.7;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTAAARV 9
|:|||||:
Db 7 ASLAAARV 15

RESULT 4
S56849
probable membrane protein YJL073w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein HRC558; hypothetical protein J1083
C;Species: Saccharomyces cerevisiae
C;Date: 05-May-1995 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004
C;Accession: S56849; S56847; S50798; S47117; S57736
R;Rose, M.; Koetter, P.; Entian, K.D.
submitted to the Protein Sequence Database, September 1995
A;Reference number: S56848
A;Accession: S56849
A;Molecule type: DNA
A;Residues: 1-692 <ROS>
A;Cross-references: UNIPROT:P40358; EMBL:Z49348; NID:g1008228; PID:g1008229; MIPS:YJL073
R;Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
submitted to the Protein Sequence Database, September 1995
A;Reference number: S56835
A;Accession: S56847
A;Molecule type: DNA
A;Residues: 135-692 <POH>
A;Cross-references: EMBL:Z49348; MIPS:YJL073w
R;Vandenbol, M.; Durand, P.; Dion, C.; Portetelle, D.; Hilger, F.
Yeast 11, 57-60, 1995
A;Title: Sequence of a 17.1 kb DNA fragment from chromosome X of Saccharomyces cerevisia
A;Reference number: S50798; MUID:95282514; PMID:7762302
A;Accession: S50798
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 135-692 <VAN>
A;Cross-references: EMBL:Z34288; NID:9498992; PIDN:CAA84049.1; PID:g498993
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1994
R;Vandenbol, M.; Durand, P.; Dion, C.; Portetelle, D.; Hilger, F.
submitted to the EMBL Data Library, June 1994
A;Description: Sequence analysis of a 17.1 kb DNA fragment from chromosome X of Saccharo
A;Reference number: S47117

A;Accession: S47117
A;Molecule type: DNA
A;Residues: 135-692 <VAW>
A;Cross-references: EMBL:Z34288; NID:g498992; PID:g498993
R;Sor, F.J.
submitted to the EMBL Data Library, June 1995
A;Reference number: S57731
A;Accession: S57736
A;Molecule type: DNA
A;Residues: 1-692 <SOR>
A;Cross-references: EMBL:X88851; NID:g895892; PID:g895898
C;Genetics:
A;Gene: SGD:JEM1
A;Cross-references: SGD:S0003609; MIPS:YJL073w
A;Map position: 10L
C;Keywords: transmembrane protein
F;585-655/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 70.0%; Score 35; DB 2; Length 692;
Best Local Similarity 70.0%; Pred. No. 45;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SIAAARVLDY 11
|:|||||:
Db 245 SLAAAILDY 254

RESULT 5
AE1210
teichoic acid biosynthesis protein B homolog lmo1085 [imported] - Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AE1210
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.;
D.; Jones, L.M.; Karet, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AB1210
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-696 <GLA>
A;Cross-references: UNIPROT:Q8Y833; GB:NC_003210; PIDN:CAC99163.1; PID:g16410487; GSPDB:(
C;Genetics:
A;Experimental source: strain EGD-e
A;Gene: lmo1085

Query Match 70.0%; Score 35; DB 2; Length 696;
Best Local Similarity 75.0%; Pred. No. 45;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AAARVLDY 11
|:|||||:
Db 685 AAARIIDY 692

RESULT 6
DB87715
carboxymethylenebutenolidase [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: DB87715
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: AB7249; MUID:21173698; PMID:11259647
A;Accession: DB87715
A;Status: preliminary

A:Molecule type: DNA
A:Residues: 1-231 <STO>
A:Cross-references: UNIPROT:Q9A213; GB:AE005673; NID:g13425534; PIDN:AAK25720.1; GSPDB:C
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T38883
C:Superfamily: carboxymethylenebutenolidase

Query Match 68.0%; Score 34; DB 2; Length 231;
Best Local Similarity 80.0%; Pred. No. 23;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ASIAAARVLD 10
|:|||||:
Db 100 ATIAAARKLD 109

RESULT 7
SUMYTV
thermitase (EC 3.4.21.66) - Thermoactinomyces vulgaris
C:Species: Thermoactinomyces vulgaris
C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004
C:Accession: A00973
R:McLoun, B.; Baudys, M.; Koetka, V.; Hausdorf, G.; Frommel, C.; Hohne, W.E.
FEBS Lett. 183, 195-200, 1985
A:Title: Complete primary structure of thermitase from Thermoactinomyces vulgaris and its
A:Reference number: A00973
A:Accession: A00973
A:Molecule type: protein
A:Residues: 1-279 <MEL>
A:Cross-references: UNIPROT:P04072
C:Comment: This protein is enzymatically similar to a proteinase from Streptomyces sp.
C:Superfamily: subtilisin; subtilisin homology
C:Keywords: hydrolase; serine proteinase
F:29-239/Domain: subtilisin homology <SBT>
F:38,71,225/Active site: Asp, His, Ser #status predicted

Query Match 68.0%; Score 34; DB 1; Length 279;
Best Local Similarity 80.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASIAAARVLD 10
|:|||||:
Db 96 ASILAVRVLD 105

RESULT 8
I40371
methyltransferase - Bacillus stearothermophilus (fragment)
C:Species: Bacillus stearothermophilus
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C:Accession: I40371
R:Rina, M.; Markaki, M.; Bouriotis, V.
Gene 150, 71-73, 1994
A:Title: Sequence of the cloned bseCIM gene: M.BaeCI reveals high homology to M.BanIII.
A:Reference number: I40371; MUID:95047552; PMID:7959066
A:Accession: I40371
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-579 <RES>
A:Cross-references: UNIPROT:P43423; EMBL:X79509; NID:g619638; PIDN:CAAS6041.1; PID:g6196
C:Genetics:
C:Superfamily: site-specific methyltransferase (adenine-specific) Paer71

Query Match 68.0%; Score 34; DB 2; Length 579;
Best Local Similarity 54.5%; Pred. No. 60;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ASIAAARVLDY 11
|:|||||:
Db 26 AEVIKRIILDY 36

RESULT 9

T38883

hypothetical protein SPAC4H3.03c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T38883

R:Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, February 1996
A:Reference number: Z21807
A:Accession: T38883

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-649 <MUR>

A:Cross-references: UNIPROT:Q10211; EMBL:Z69380; PIDN:CAA93342.1; GSPDB:GN00066; SPDB:SPY
A:Experimental source: strain 972h-; cosmid c4H3
C:Genetics:

A:Gene: SPDB:SPAC4H3.03c

A:Map position: 1

C:Superfamily: Schizosaccharomyces pombe hypothetical protein SPAC4H3.03c

Query Match 68.0%; Score 34; DB 2; Length 649;

Best Local Similarity 70.0%; Pred. No. 68;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ASIAAARVLD 10

|:|||||:
Db 631 AAIAAAHILD 640

RESULT 10

B71468

probable insulinase family/proteinase III - Chlamydia trachomatis (serotype D, strain UW)
C:Species: Chlamydia trachomatis
C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C:Accession: B71468

R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trach
A:Reference number: A71570; MUID:99000809; PMID:9784136
A:Accession: B71468

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-956 <ARN>

A:Cross-references: UNIPROT:O84812; GB:AE001353; GB:AE001273; NID:g3329271; PIDN:AAC6840

A:Experimental source: serotype D, strain UW-3/Cx

C:Genetics:

A:Gene: ptr

C:Superfamily: insulin-degrading enzyme (IDE)

Query Match 68.0%; Score 34; DB 2; Length 956;

Best Local Similarity 77.8%; Pred. No. 1e+02;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 IAAARVLDY 11

|:|||||:
Db 916 IAAARSNDY 924

RESULT 11

AF1059

probable transcription regulator STY4801 [imported] - Salmonella enterica subsp. enterica
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AF1059

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
Th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A:Reference number: AB0502; MUID:21534947; PMID:11677608

A:Accession: AF1059

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-162 <PAR>
A:Cross-references: GB:ALS13382; PIDN:CAD06923.1; PID:gl505571; GSPDB:GN00176
C:Genetics:
A:Gene: STY4801

Query Match 66.0%; Score 33; DB 2; Length 162;
Best Local Similarity 75.0%; Pred. No. 26;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 ASIAARVLDY 11
|||||
Db 112 AVARILDY 119

RESULT 12
AF2831
DNA polymerase III, epsilon subunit [imported] - Agrobacterium tumefaciens (strain C58,
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AF2831
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Kreepan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AF2831
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-202 <KUR>
A:Cross-references: UNIPROT:Q8UDP4; GB:AE008688; PIDN:AAL43068.1; PID:gl7740536; GSPDB:G
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu2077
A:Map position: circular chromosome

Query Match 66.0%; Score 33; DB 2; Length 202;
Best Local Similarity 88.9%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASIAARVLDY 9
|||||
Db 156 ASIAARAL 164

RESULT 13
B97609
Probable DNA polymerase III, epsilon chain [imported] - Agrobacterium tumefaciens (strain
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C:Accession: B97609
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorllo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: B97609
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-202 <KUR>
A:Cross-references: UNIPROT:Q8UDP4; GB:AE007869; PIDN:AAK87827.1; PID:gl5157207; GSPDB:G
C:Genetics:
A:Gene: AGR_C 3764
A:Map position: circular chromosome

Query Match 66.0%; Score 33; DB 2; Length 202;
Best Local Similarity 88.9%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASIAARVLDY 9
|||||
Db 156 ASIAARAL 164

RESULT 14
F89878
conserved hypothetical protein SA0939 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: F89878
R;Kuroda, M.; Onca, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaico, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: F89878
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-220 <KUR>
A:Cross-references: UNIPROT:Q99V10; GB:BA000018; PID:gl3700889; PIDN:BAB42185.1; GSPDB:GN
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA0939
C:Superfamily: conserved hypothetical protein MG323

Query Match 66.0%; Score 33; DB 2; Length 220;
Best Local Similarity 60.0%; Pred. No. 35;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 SIAAARVLDY 11
:||:|
Db 131 NVASASVLDY 140

RESULT 15
G69213
hypothetical protein MTH852 - Methanobacterium thermoautotrophicum (strain Delta H)
C:Species: Methanobacterium thermoautotrophicum
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: G69213
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; E
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.;
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functi
A:Reference number: A69000; MUID:98037514; PMID:9371463
A:Accession: G69213
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-264 <MTH>
A:Cross-references: UNIPROT:O26940; GB:AE000862; GB:AE000666; NID:g2621943; PIDN:AAB85351
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH852

Query Match 66.0%; Score 33; DB 2; Length 264;
Best Local Similarity 54.5%; Pred. No. 43;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASIAAARVLDY 11
|||||
Db 94 ASIAAVKLIN 104

Search completed: October 14, 2005, 16:23:38
Job time : 17.2969 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2005, 15:51:44 ; Search time 73.2188 Seconds
(without alignments)
76.932 Million cell updates/sec

Title: US-10-614-959-12
Perfect score: 50
Sequence: 1 ASIAAARVLDY 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03.*
1: uniprot_spot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	37	74.0	421	2	Q6H820	Q6h820 oryza sativ
2	37	74.0	694	2	Q8EFS2	Q8efe2 shewanella
3	37	74.0	1203	2	Q8S2E4	Q8s2e4 oryza sativ
4	37	74.0	1234	2	Q8GU81	Q8gu81 oryza sativ
5	36	72.0	402	2	Q62CX8	Q62cx8 burkholderi
6	36	72.0	402	2	Q63M18	Q63m18 burkholderi
7	36	72.0	663	2	Q8UA95	Q8ua95 agrobacteri
8	36	72.0	709	2	Q7CSK5	Q7csk5 agrobacteri
9	36	72.0	723	2	Q8H034	Q8h034 oryza sativ
10	36	72.0	778	2	Q7MA36	Q7ma36 wolfinella s
11	36	72.0	1072	2	Q69X93	Q69x93 oryza sativ
12	35	70.0	143	2	Q69582	Q69582 human herpe
13	35	70.0	184	2	Q6AQ91	Q6aq91 desulfotale
14	35	70.0	329	2	Q9RJ77	Q9rj77 streptomyc
15	35	70.0	692	1	YJH3_YEAST	P40358 saccharomyc
16	35	70.0	696	2	Q8Y833	Q8y833 listeria mo
17	35	70.0	1228	2	Q8MK31	Q8mk31 bdellovibri
18	35	70.0	6977	2	Q7R034	Q7r034 giardia lam
19	34	68.0	153	2	Q6NA42	Q6na42 rhodospseud
20	34	68.0	231	2	Q9A213	Q9a213 caulobacter
21	34	68.0	279	1	THET_THEVU	P04072 thermocacti
22	34	68.0	322	2	Q6AH73	Q6ah73 leifsonia x
23	34	68.0	342	2	Q8ZSL1	Q8zsl1 pyrobaculum
24	34	68.0	342	2	Q8ZXL8	Q8zxl8 pyrobaculum
25	34	68.0	342	2	Q9LS05	Q9ls05 arabidopsis
26	34	68.0	344	2	Q9FV51	Q9fv51 arabidopsis
27	34	68.0	568	2	Q8P7L4	Q8p7l4 xanthomonas
28	34	68.0	568	2	Q8PIY6	Q8piy6 xanthomonas
29	34	68.0	579	1	MTCL_BACST	P43423 bacillus st
30	34	68.0	579	2	Q9RQK2	Q9rqk2 bacillus st
31	34	68.0	589	2	Q7F1D1	Q7f1d1 oryza sativ

32 34 596 2 Q7QH89 anopheles g
33 34 649 1 YAY3_SCHPO Q10211 schizosacch
34 34 827 2 Q6ZG00 Q6z900 oryza sativ
35 34 866 2 Q6FY30 Q6fy30 candida gla
36 34 874 2 Q67R60 Q67r60 symbiobacte
37 34 880 2 Q8ZW19 Q8zw19 pyrobaculum
38 34 912 2 Q8A1R0 Q8a1r0 bacteroides
39 34 945 2 Q7EZJ3 Q7ezj3 oryza sativ
40 34 956 2 Q84812 Q84812 chlamydia t
41 34 1206 2 Q8ZXP1 Q8zxp1 pyrobaculum
42 34 68.0 2 Q8ZVB9 Q8zvb9 pyrobaculum
43 33 66.0 162 2 Q82129 Q82129 salmonella
44 33 66.0 162 2 Q8ZK37 Q8zk37 salmonella
45 33 66.0 162 2 Q83SS1 Q83ss1 salmonella

ALIGNMENTS

RESULT 1

Q6H820 PRELIMINARY; PRT; 421 AA.
ID Q6H820;
AC Q6H820;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE GCN5-related N-acetyltransferase-like.
GN Name=QJ1297.C09.4;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP004087; BAD25129.1; -.
DR GO; GO:0008080; F:N-acetyltransferase activity; IEA.
DR GO; GO:0016740; P:transferase activity; IEA.
DR InterPro; IPR000182; GCN5acetyl trans.
DR InterPro; IPR000504; RNA rec.mot.
DR Pfam; PF00583; Acetyltransf_1; 1.
DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
KW Transferase.
SQ SEQUENCE 421 AA; 44979 MW; 7A9968BFFC673920 CRC64;

Query Match 74.0%; Score 37; DB 2; Length 421;
Best Local Similarity 80.0%; Pred. No. 69;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASIAAARVLD 10
||:|||||
Db 288 ASLAARALD 297

RESULT 2

Q8EFS2 PRELIMINARY; PRT; 694 AA.
ID Q8EFS2;
AC Q8EFS2;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 26, Last annotation update)
DE Acetyl-CoA carboxylase, biotin carboxylase, putative.
GN OrderedLocusNames=SQ1894;
OS Shewanella oneidensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Shewanellaceae; Shewanella.
OX NCBI_TaxID=70863;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MR-1;
RC STRAIN=MR-1;
MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;

Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
Zhong H., Iwana H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
Yano M., Jiang J., Gojobori T.,
"The genome sequence and structure of rice chromosome 1.";
Nature 420:312-316(2002).
-1- SIMILARITY: Belongs to the ABC transporter family.
EMBL; AF003229; BAB89499.1; -.
DR HSSP; P08716; 1MT0.
DR GRamene; Q8S2E4; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0043626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR011527; ABC_TM_transp.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00664; ABC_membrane_2.
DR Pfam; PF00005; ABC_tran; 2.
DR ProDom; PD000006; ABC_transporter; 2.
DR SMART; SM00382; AAA; 2.
DR PROSITE; PS0929; ABC_TM1F; 2.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 2.
DR PROSITE; PS0893; ABC_TRANSPORTER_2; 2.
ATP-binding.
KW ATP-binding.
SQ SEQUENCE 1203 AA; 131506 MW; B7838BDC1B5F19AA CRC64;
Query Match 74.0%; Score 37; DB 2; Length 1203;
Best Local Similarity 70.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 ASTAAARVLD 10
||:|:|:
DB 330 ASVAATRIID 339
RESULT 4
Q8GU81 PRELIMINARY; PRT; 1234 AA.
ID Q8GU81
AC Q8GU81;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
MDR-like ABC transporter.
GN Names=mdr17;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OC NCBI_TaxID=39947;
[1]
RN SEQUENCE FROM N.A.
RP Jasinaki M., Ducos E., Martinoia E., Boutry M.;
RA "the ATP-binding cassette transporters: structure, function and gene
RT family comparison between rice and Arabidopsis.";
RL Plant Physiol. 0:0-0(0).
[2]
RN SEQUENCE FROM N.A.
RP Ducos E.;
RA Submitted (NOV-2002) to the EMBL/GenBank/DBAJ databases.
RL -1- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AJ35055; CAD59577.1; -.
DR HSSP; P08716; 1MT0.
DR GRamene; Q8GU81; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR011527; ABC membrane 1.
DR InterPro; IPR001140; ABC_TM_transp.

PubMed=15377794;
 RX Holden M.T.G., Titball R.W., Peacock S.J., Cardeno-Tarraga A.M.,
 RA Atkins I., Crossman L.C., Pitt T., Churcher C., Mungall K.,
 RA Bentley S.D., Sebaihia M., Thomson N.R., Bason N., Beacham I.R.,
 RA Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
 RA Chillingworth T., Cronin A., Cresset B., Davis P., DeShazer D.,
 RA Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagsels K.,
 RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
 RA Rabinowitz E., Rutherford K., Sanders M., Simmonds M.,
 RA Songailavicius S., Stevens K., Tumapa S., Vesaratchaveest M.,
 RA Whitehead S., Yeates C., Barrell B.G., Oyston P.C.F., Parkhill J.,
 RT "Genomic plasticity of the causative agent of melioidosis,
 RK Burkholderia pseudomallei";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
 DR EMBL; BX571966; CAH3804.1; -.
 SQ SEQUENCE 402 AA; 41596 MW; 6FCA16BE0F4B18EA CRC64;

Query Match 72.0%; Score 36; DB 2; Length 402;
 Best Local Similarity 70.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASIAAARVLD 10
 ||:|||||
 Db 106 ATVAARLDD 115

RESULT 7
 Q8UA95 PRELIMINARY; PRT; 663 AA.
 ID Q8UA95;
 AC Q8UA95;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE 3-methylcrotonyl-CoA carboxylase alpha subunit.
 GN Name=mccaA; OrderedLocusNames=Atu3479;
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
 OX NCBI_TaxID=176299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Dupont;
 RX MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;
 RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
 RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
 RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
 RA Chapman P., Clendinning J., Deatherage G., Gillet W., Grant C.,
 RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
 RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
 RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
 RA Nester E.W.,
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
 C58";
 RL Science 294:2317-2323(2001).
 DR EMBL; AE009278; AAL44292.1; -.
 DR PIR; A98299; A98299.
 DR PIR; AF2984; AF2984.
 DR HSP; P24182; IBNC.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0009374; F:biotin binding; IEA.
 DR GO; GO:0016874; F:ligase activity; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR Pfam; PF02785; Biotin carb C; 1.
 DR Pfam; PF00364; Biotin_lipoYL; 1.
 DR Pfam; PF00289; CPSase_L_chain; 1.
 DR PROSITE; PS00188; BIOTIN; 1.
 DR PROSITE; PS00866; CPSASE_1; UNKNOWN_1.
 DR PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
 KW Biotin; Complete proteome.
 SQ SEQUENCE 663 AA; 71187 MW; 2366201C5F36D292 CRC64;

InterPro; IPR003439; ABC_transporter.
 DR Pfam; PF00664; ABC_membrane; 2.
 DR Pfam; PF00005; ABC_tran; 2.
 DR ProDom; PD000006; ABC_transporter; 2.
 DR SMART; SM00382; AAA; 2.
 DR PROSITE; PS00929; ABC_TWIF; 2.
 DR PROSITE; PS00211; ABC_TRANSPORTER_1; 2.
 DR PROSITE; PS00893; ABC_TRANSPORTER_2; 2.
 KW ATP-binding.
 SQ SEQUENCE 1234 AA; 134571 MW; C5F9E9D75D28AC93 CRC64;

Query Match 74.0%; Score 37; DB 2; Length 1234;
 Best Local Similarity 70.0%; Pred. No. 2e+02;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASIAAARVLD 10
 ||:|||||
 Db 330 ASVAATRLD 339

RESULT 5
 Q62CX8 PRELIMINARY; PRT; 402 AA.
 ID Q62CX8;
 AC Q62CX8;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Major facilitator superfamily protein.
 GN ORFNames=BMA0712;
 OS Burkholderia mallei ATCC 23344.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Burkholderia.
 OX NCBI_TaxID=243160;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 23344;
 RA Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
 RA Feldblyum T., Ulrich R.L., Ronning C.M., Brinkac L.M., Daugherty S.C.,
 RA Davidson T.D., Deboy R.T., Dimitrov G., Dodson R.J., Durkin A.S.,
 RA Gwinn M.L., Haft D.H., Khouri H., Kolonay J.F., Madupu R.,
 RA Mohammad Y., Nelson W.C., Radune D., Romero C.M., Sarria S.,
 RA Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y., Zafar N.,
 RA Zhou L., Fraser C.M.,
 RT "Structural flexibility in the Burkholderia mallei genome";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:14247-14251(2004).
 DR EMBL; CP000011; AAU46877.1; -.
 SQ SEQUENCE 402 AA; 41596 MW; 6FCA16BE0F4B18EA CRC64;

Query Match 72.0%; Score 36; DB 2; Length 402;
 Best Local Similarity 70.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASIAAARVLD 10
 ||:|||||
 Db 106 ATVAARLDD 115

RESULT 6
 Q63M18 PRELIMINARY; PRT; 402 AA.
 ID Q63M18;
 AC Q63M18;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Putative transporter protein.
 GN ORFNames=BPSS0842;
 OS Burkholderia pseudomallei K96243.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Burkholderia.
 OX NCBI_TaxID=272560;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K96243;
 RX

Query Match 72.0%; Score 36; DB 2; Length 663;
Best Local Similarity 63.6%; Pred. No. 1.7e+02;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASIAAARVLDY 11
DB 258 AATAAARAIDY 268
|:|||||:|

RESULT 8
Q7CSK5 PRELIMINARY; PRT; 709 AA.

ID Q7CSK5
AC Q7CSK5
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE AGR_L_2704P
GN OrderedLocNames=AGR_L_2704;
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=Cereon;
RX MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1065803;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Houmial K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58.";
RL Science 294:2323-2328(2001).
DR EMBL; AE008334; AAK89915.1; --
DR HSSP; P02905; 1BDO.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0009374; F:biotin binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR001882; Biotin_BS
DR InterPro; IPR005482; Biotin_carb_C.
DR InterPro; IPR000089; Biotin_lipoyL.
DR InterPro; IPR005481; CPase_L_N.
DR InterPro; IPR005479; Cph synth L D2.
DR InterPro; IPR011053; Hybrid motif.
DR InterPro; IPR011054; Rudmt_hyb_motif.
DR Pfam; PF02785; Biotin_card_C; 1.
DR Pfam; PF00364; Biotin_lipoyL; 1.
DR Pfam; PF00289; CPase_L_chain; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR PROSITE; PS00866; CPASE_1; UNKNOWN_1.
DR PROSITE; PS00867; CPASE_2; UNKNOWN_1.
KW Biotin.
SQ SEQUENCE 709 AA; 76278 MW; 1F43A1F1919BF00 CRC64;

Query Match 72.0%; Score 36; DB 2; Length 709;
Best Local Similarity 63.6%; Pred. No. 1.8e+02;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASIAAARVLDY 11
DB 304 AATAAARAIDY 314
|:|||||:|

RESULT 9
Q8H034 PRELIMINARY; PRT; 723 AA.

ID Q8H034
AC Q8H034
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

Hypothetical protein OJ1172F09.9.
GN Name=OJ1172F09.9;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
[1]
RN SEQUENCE FROM N.A.
RP Wing R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Currie J.,
RA Collura K., McCombie D.W.R., de la Bastide M., Spiegel L., Preston R.,
RA Kirchoff K., Kuit K., Nascimento L., Zutavern T., Salija V., Bell M.,
RA Baker J., Santos L., Miller B., Katzenberger F., Muller S., King L.,
RA Yang C., O'Shaughnessy A., Palmer L., Dedhia N.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; ACL19796; AAC17354.1; --
DR Gramene; Q8H034; --
DR InterPro; IPR008938; ARM.
DR Hypothetical protein.
SQ SEQUENCE 723 AA; 78613 MW; 3FD8422158ED1DF CRC64;

Query Match 72.0%; Score 36; DB 2; Length 723;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASIAAARVLD 10
DB 616 ASIAAARVTD 625
|:|||||:|

RESULT 10
Q7MA36 PRELIMINARY; PRT; 778 AA.

ID Q7MA36
AC Q7MA36; 2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE FLAGELLAR FUNCTIONAL PROTEIN.
GN Name=PFLA; OrderedLocNames=WS0490;
OS Wolinella succinogenes.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Wolinella.
OX NCBI_TaxID=844;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=DSM 1740;
RX MEDLINE=22882897; PubMed=14500908; DOI=10.1073/pnas.1932838100;
RA Baar C., Eppinger M., Raddatz G., Simon J., Lanz C., Klimmek O.,
RA Nandakumar R., Gross R., Rosinus A., Keller H., Jagtap P., Linke B.,
RA Meyer F., Lederer H., Schuster S.C.;
RT "Complete genome sequence and analysis of Wolinella succinogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:11690-11695(2003).
DR EMBL; BX571658; CAE09628.1; --
DR GO; GO:0019861; C:flagellum; IEA.
DR InterPro; IPR008940; Prenyl_trans.
DR InterPro; IPR001440; TPR.
DR InterPro; IPR008941; TPR-like.
DR Pfam; PF00515; TPR_1; 1.
DR PROSITE; PS50293; TPR_REGION; 1.
KW Complete proteome; Flagellum.
SQ SEQUENCE 778 AA; 89775 MW; 3E2F992CE949C27E CRC64;

Query Match 72.0%; Score 36; DB 2; Length 778;
Best Local Similarity 63.6%; Pred. No. 2e+02;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASIAAARVLDY 11
DB 322 ASIAAARVLDY 332
|:|||||:|

RESULT 11
Q69X93

```

ID Q69X93 PRELIMINARY; PRT; 1072 AA.
AC Q69X93;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative receptor-like protein kinase 2.
GN Names:P06333E08.13;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoae; Oryza.
OC NCBI_TaxID=39947;
RN [1]
SEQUENCE FROM N.A.
RA Sabaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GAS) genomic DNA, chromosome 6, PAC
clone:P06333E08.13";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR DR EMBL; AP003622; BAD32908.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR007090; LRR_plant.
DR InterPro; IPR003591; LRR_typ.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; PS002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_kin_AS.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00560; LRR_1; 22.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00369; LRR_TYF; 11.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
KW Transferase.
SQ SEQUENCE 1072 AA; 114368 MW; E15B809971B15F78 CRC64;

Query Match 72.0%; Score 36; DB 2; Length 1072;
Best Local Similarity 80.0%; Pred. No. 2.7e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASIAAARVLD 10
Db 116 ASLAARVLD 125

RESULT 12
Q69582 PRELIMINARY; PRT; 143 AA.
AC Q69582;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Herpesvirus Type 6 DNA.
OS Human herpesvirus 6.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Roseolovirus.
OC NCBI_TaxID=10368;
RN [1]
SEQUENCE FROM N.A.
RA Thompson J., Choudhury S., Kashanchi F., Doniger J., Berneman Z.,
RA Frenkel N., Rosenthal L.J.;

ID Q69J97 PRELIMINARY; PRT; 329 AA.
AC Q69J97;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative zinc-binding oxidoreductase.
GN ORFNames:SCF51.18;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OC NCBI_TaxID=1902;
RN [1]
SEQUENCE FROM N.A.
RA STRAIN=A3 (2) / M145;

RT "A transforming fragment within the direct repeat region of human
herpesvirus type 6 that transactivates HIV-1.";
RL Oncogene 9:1167-1175(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Thompson J.T.;
RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; X73675; CAAS2028.1; -.
DR PIR; S43071; S43071.
SQ SEQUENCE 143 AA; 13317 MW; EDF78898C3D31734 CRC64;

Query Match 70.0%; Score 35; DB 2; Length 143;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASIAAARVLD 9
Db 7 ASLAARVLD 15

RESULT 13
Q6A091 PRELIMINARY; PRT; 184 AA.
AC Q6A091;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=DP0753;
OS Desulfotalea psychrophila.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacteriales;
OC Desulfobulbaceae; Desulfotalea.
OC NCBI_TaxID=84980;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=LS954 / DSM 12343;
RX PubMed=15305914;
RA Rabus R., Ruepp A., Frickey T., Rattei T., Partmann B., Stark M.,
RA Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K.,
RA Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,
RA Klenk H.-P.;
RT "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
from permanently cold Arctic sediments.";
RL Environ. Microbiol. 6:887-902(2004).
DR EMBL; CR522870; CAG35482.1; -.
KW Complete proteome.
SQ SEQUENCE 184 AA; 20792 MW; 8D9DCB5EDFAA60AF CRC64;

Query Match 70.0%; Score 35; DB 2; Length 184;
Best Local Similarity 80.0%; Pred. No. 81;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASIAAARVLD 10
Db 99 ASIAAARVLD 108

RESULT 14
Q9RJ97 PRELIMINARY; PRT; 329 AA.
AC Q9RJ97;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative zinc-binding oxidoreductase.
GN ORFNames:SCF51.18;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OC NCBI_TaxID=1902;
RN [1]
SEQUENCE FROM N.A.
RA STRAIN=A3 (2) / M145;
```

RA MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RX Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kiese H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kiese H., Kiese T., Larke L., Murphy L.D., Oliver K., O'Neil S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wierozorek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL939105; CAB59716.1; -.
DR HSP; Q8L3C8; ILYZ.
DR GO; GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR002085; Adh zn family.
DR InterPro; IPR011032; GroES like.
DR Pfam; PF00107; ADH_zinc_N; 1.
KW Complete proteome.
SQ SEQUENCE 329 AA; 34155 MW; SDCADAFBI174FD042 CRC64;

Query Match 70.0%; Score 35; DB 2; Length 329;
Best Local Similarity 70.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SIAAARVLDY 11
|:|:|:|:|
Db 189 SLGAARVLDY 198

RESULT 15
YOH3_YEAST
ID YOH3_YEAST STANDARD; PRT; 692 AA.
AC P40358;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypothetical 80.4 kDa protein in SMC3-MRPL8 intergenic region.
GN OrderedLocusNames=YJL073W; ORFNames=YJL083, HRC558;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Rose M., Koetter P., Entian K.D.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RA Sor F.J.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 135-692 FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=95282514; PubMed=7762302;
RA Vandenbol M., Durand P., Dion C., Portetelle D., Hilger F.;
RT "Sequence of a 17.1 kb DNA fragment from chromosome X of Saccharomyces
RT cerevisiae includes the mitochondrial ribosomal protein L8.";
RL Yeast 11:57-60(1995).
CC -1- SIMILARITY: Contains 1 J domain.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL; Z49348; CAA89365.1; -.

DR EMBL; X88851; CAA61312.1; -.
DR EMBL; Z34288; CAA84049.1; -.
DR PIR; S56849; S56849.
DR HSP; P08622; 1BQZ.
DR Germonline; 141687; -.
DR SGD; S00003609; JEM1.
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR GO; GO:0003000; C:peripheral to membrane of membrane fraction; IDA.
DR GO; GO:0003767; F:co-chaperone activity; IGI.
DR GO; GO:0000742; P:karyogamy during conjugation with cellular . . .; IGI.
DR GO; GO:0006457; P:protein folding; IGI.
DR InterPro; IPR001623; DnaJ_N.
DR Pfam; PF00226; DnaJ; 1.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00636; DNAJ_1; FALSE_NEG.
DR PROSITE; PS00076; DNAJ_2; 1.
KW Hypothetical protein.
FT DOMAIN 560 569 Poly-Gln.
FT DOMAIN 585 655 J-domain.
SQ SEQUENCE 692 AA; 80381 MW; 9F612DD16B66981B CRC64;

Query Match 70.0%; Score 35; DB 1; Length 692;
Best Local Similarity 70.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SIAAARVLDY 11
|:|:|:|:|
Db 245 SLAAAIILDY 254

Search completed: October 14, 2005, 16:19:53
Job time : 75.2188 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2005, 15:51:19 ; Search time 99.9375 Seconds
(without alignments)
50.310 Million cell updates/sec

Title: US-10-614-959-13
Perfect score: 66
Sequence: 1 SGSTNIGNNYYVS 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	66	100.0	13	3	AAY79071 Anti-fact
2	66	100.0	109	4	Aau02544 Anti-adip
3	66	100.0	110	4	Aau02558 Anti-adip
4	66	100.0	110	4	Aau02612 Anti-adip
5	66	100.0	110	4	Aau02627 Anti-adip
6	66	100.0	110	4	Aau02629 Anti-adip
7	66	100.0	111	4	Aau02542 Anti-adip
8	66	100.0	111	4	Aau02551 Anti-adip
9	66	100.0	240	5	Abp45887 Human Bly
10	66	100.0	240	7	Adg96714 Single ch
11	66	100.0	242	8	Adg34301 Neurokini
12	66	100.0	242	8	Adg34317 Neurokini
13	66	100.0	243	5	Abp45916 Human Bly
14	66	100.0	243	6	Aao31147 Human CMO
15	66	100.0	243	7	Adg96743 Single ch
16	66	100.0	243	8	Adg34310 Neurokini
17	66	100.0	243	8	Adg34306 Neurokini
18	66	100.0	244	5	Adg34303 Neurokini
19	66	100.0	245	8	Abp45915 Human Bly
20	66	100.0	245	7	Adg96742 Single ch
21	66	100.0	245	7	Adg98057 TNF proli
22	66	100.0	245	8	Adg83862 Chemokine
23	66	100.0	245	8	Adg34308 Neurokini
24	66	100.0	245	8	Adg34313 Neurokini
25	66	100.0	246	5	Abp45902 Human Bly

26	66	100.0	246	5	Abp45906 Human Bly
27	66	100.0	246	7	Adg96733 Single ch
28	66	100.0	246	7	Adg96729 Single ch
29	66	100.0	246	8	Adg83872 Chemokine
30	66	100.0	247	5	Abp45671 Human Bly
31	66	100.0	247	5	Abp45432 Human Bly
32	66	100.0	247	5	Abp45923 Human Bly
33	66	100.0	247	5	Abp45917 Human Bly
34	66	100.0	247	5	Abp45696 Human Bly
35	66	100.0	247	5	Abp45888 Human Bly
36	66	100.0	247	7	Adg30413 Human GMB
37	66	100.0	247	7	Adg30455 Human GMB
38	66	100.0	247	7	Adg96715 Single ch
39	66	100.0	247	7	Adg96498 Single ch
40	66	100.0	247	7	Adg96744 Single ch
41	66	100.0	247	7	Adg96259 Single ch
42	66	100.0	247	7	Adg96750 Single ch
43	66	100.0	247	8	Adg96523 Single ch
44	66	100.0	247	8	Adg83874 Chemokine
45	66	100.0	247	8	Adg34304 Neurokini

ALIGNMENTS

RESULT 1
AAY79071
ID AAY79071 standard; peptide; 13 AA.
XX
AC AAY79071;
XX
DT 12-JUN-2000 (first entry)
XX
DE Anti-factor IX/IXa antibody L chain V domain CDR1 amino acid sequence.
XX
KW Complementarity determining region 1; CDR1; antibody; Gla domain;
KW factor IX/IXa; blood coagulation; deep venous thrombosis; light chain;
KW arterial thrombosis; unstable angina; post myocardial infarction;
KW coronary artery bypass graft; CABG; stroke; tumour growth; metastasis;
KW percutaneous transluminal coronary angioplasty; PTCA; inflammation;
KW septic shock; hypotension; adult respiratory distress syndrome; ARDS;
KW arterial fibrillation; disseminated intravascular coagulopathy; DIC.
XX
OS Homo sapiens.
XX
FN WO200012562-A1.
XX
PD 09-MAR-2000.
XX
PF 26-AUG-1999; 99WO-US019453.
XX
PR 28-AUG-1998; 98US-0098233P.
XX
PR 03-MAR-1999; 99US-0122767P.
XX
PA (GETH) GENENTECH INC.
XX
PI Adams CW, Devaux B, Eaton DL, Hass PE, Judice JK, Kirchhofer D;
PI Suggett S;
XX
WPI; 2000-256595/22.
XX
PT Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-
PT carboxyglutamic acid domains useful as anti-coagulant in thrombosis,
PT stroke, and post myocardial infarction.
XX
PS Claim 8; Fig 2; 84pp; English.
XX
CC This sequence represents a complementarity determining region 1 (CDR1) of
CC the light chain variable domain of a human anti-factor IX/IXa Gla domain
CC antibody. Factor IXa is a vitamin K dependent plasma serine protease that
CC participates in the blood coagulation pathways. The Gla domain of factor
CC IXa and its zymogen factor IX contains important structural determinants
CC for interaction with high affinity binding sites on vascular endothelial

Qy	1	SGSTSNIGNNYVS	13
Dd	23	SGSTSNIGNNYVS	35

RESULT 3
AAU02558
ID AAU02558 standard; protein: 110 AA.

XX	
AC	AAU02558;
XX	
DT	29-AUG-2001 (first entry)

DE	Anti-adipocyte monoclonal antibody light chain, FAT 44.
XX	
XX	Antibody; adipocyte; heavy chain; light chain; obesity; fat;
KW	heart disease; complementarity determining region; CDR.
KW	
XX	
XX	Homo sapiens.
OS	
XX	
XX	WC200127279-A1.
PN	
XX	
XX	19-APR-2001.
PD	
XX	
XX	11-OCT-2000; 2000WO-GB003900.
PF	

PR 12-OCT-1999; 99US-0158812P.
XX
XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Edwards BM, Main SH, Vaughan TJ;
XX
XX WPI; 2001-282031/29.
DR
DR N-ESDB; AAS03458.
XX
XX
XX Panel of specific binding members of antibody molecules which bind to
PT whole adipocytes is used in the treatment of obesity and obesity related
PT diseases.
XX
XX Claim 1; Page 128-129; 182pp; English.
PS
PS
XX
XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC

and heavy chain complementarity determining regions (CDR) of the invention. The antibodies can be used in the treatment of obesity and obesity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the fat mass of an obese patient or the antibody can be used as a therapeutic itself. Antibodies binding specifically to the CDR3 region of the heavy chain can be used to deliver the cell

by complement mediated lysis. The antibodies may be labeled with a detectable label such as radiolabel, fluorescent or chemical group and used in methods of diagnosis in human subjects e.g. to determine the presence of adipocyte antigen on the surface of an adipocyte to detect or determine the presence or level of adipocytes in a cell or tissue sample. The antibodies can be used as an alternative means of treatment for obese patients other than undergoing surgery to remove excess fat. Antibodies for different types of fat deposits can also be produced e.g. intra-abdominal fat associated with heart disease

Sequence 110 AA;

Query Match 100.0%; Score 66; DB 4; Length 110;
Post-Translational Similarity 100.0%; Pred. No. 0.0026;

Query Match	100.0%;	Score 66;	DB 4;	Length 110;
Best Local Similarity	100.0%;	Pred. No. 0.0026;		
Matches	12.	Conservative	0.	Mismatches 0;
				Indels 0;
				Gaps 0

AAU02627 standard; protein; 110 AA.
 AAU02627;
 29-AUG-2001 (first entry)
 Anti-adipocyte monoclonal antibody light chain, FAT 112.
 Antibody; adipocyte; heavy chain; light chain; obesity; fat;
 heart disease; complementarity determining region; CDR.
 Homo sapiens.
 WO200127279-A1.
 19-APR-2001.
 11-OCT-2000; 2000WO-GB003900.
 12-OCT-1999; 99US-0158812P.
 (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 Edwards BM, Main SH, Vaughan TJ;
 WPI; 2001-282031/29.
 N-PSDB; AAS03527.
 Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related diseases.
 Claim 1; Page 172; 182pp; English.
 AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid sequences of anti-adipocyte monoclonal antibody heavy chain, light chain, and heavy chain complementarity determining regions (CDR) of the invention. The antibodies can be used in the treatment of obesity and obesity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the fat mass of an obese patient or the antibody can be used as a therapeutic itself. Antibodies binding specifically to adipocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a detectable label such as radiolabel, fluorescent or chemical group and used in methods of diagnosis in human subjects e.g. to determine the presence of adipocyte antigen on the surface of an adipocyte to detect or determine the presence or level of adipocytes in a cell or tissue sample. The antibodies can be used as an alternative means of treatment for obese patients other than undergoing surgery to remove excess fat. Antibodies for different types of fat deposits can also be produced e.g. intra-abdominal fat associated with heart disease
 Sequence 110 AA;
 Query Match 100.0%; Score 66; DB 4; Length 110;
 Best Local Similarity 100.0%; Pred. No. 0.0026;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 SGSTSNIGNNYVS 13
 |||||
 Db 23 SGSTSNIGNNYVS 35
 RESULT 6
 AAU02629
 ID AAU02629 standard; protein; 110 AA.
 XX
 AC AAU02629;
 XX
 29-AUG-2001 (first entry)
 Anti-adipocyte monoclonal antibody light chain, FAT 113.
 Antibody; adipocyte; heavy chain; light chain; obesity; fat;
 heart disease; complementarity determining region; CDR.
 Homo sapiens.
 WO200127279-A1.
 19-APR-2001.
 11-OCT-2000; 2000WO-GB003900.
 12-OCT-1999; 99US-0158812P.
 (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 Edwards BM, Main SH, Vaughan TJ;
 WPI; 2001-282031/29.
 N-PSDB; AAS03527.
 Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related diseases.
 Claim 1; Page 163; 182pp; English.
 AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid sequences of anti-adipocyte monoclonal antibody heavy chain, light chain, and heavy chain complementarity determining regions (CDR) of the invention. The antibodies can be used in the treatment of obesity and obesity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the fat mass of an obese patient or the antibody can be used as a therapeutic itself. Antibodies binding specifically to adipocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a detectable label such as radiolabel, fluorescent or chemical group and used in methods of diagnosis in human subjects e.g. to determine the presence of adipocyte antigen on the surface of an adipocyte to detect or determine the presence or level of adipocytes in a cell or tissue sample. The antibodies can be used as an alternative means of treatment for obese patients other than undergoing surgery to remove excess fat. Antibodies for different types of fat deposits can also be produced e.g. intra-abdominal fat associated with heart disease
 Sequence 110 AA;
 Query Match 100.0%; Score 66; DB 4; Length 110;
 Best Local Similarity 100.0%; Pred. No. 0.0026;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 SGSTSNIGNNYVS 13
 |||||
 Db 23 SGSTSNIGNNYVS 35
 RESULT 5
 AAU02627

1 SGSTSNIGNNYVS 13
 |||||
 23 SGSTSNIGNNYVS 35
 RESULT 4
 AAU02612
 ID AAU02612 standard; protein; 110 AA.
 XX
 AC AAU02612;
 XX
 29-AUG-2001 (first entry)
 Anti-adipocyte monoclonal antibody light chain, FAT 99.
 Antibody; adipocyte; heavy chain; light chain; obesity; fat;
 heart disease; complementarity determining region; CDR.
 Homo sapiens.
 WO200127279-A1.
 19-APR-2001.
 11-OCT-2000; 2000WO-GB003900.
 12-OCT-1999; 99US-0158812P.
 (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 Edwards BM, Main SH, Vaughan TJ;
 WPI; 2001-282031/29.
 N-PSDB; AAS03512.
 Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related diseases.
 Claim 1; Page 163; 182pp; English.
 AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid sequences of anti-adipocyte monoclonal antibody heavy chain, light chain, and heavy chain complementarity determining regions (CDR) of the invention. The antibodies can be used in the treatment of obesity and obesity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the fat mass of an obese patient or the antibody can be used as a therapeutic itself. Antibodies binding specifically to adipocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a detectable label such as radiolabel, fluorescent or chemical group and used in methods of diagnosis in human subjects e.g. to determine the presence of adipocyte antigen on the surface of an adipocyte to detect or determine the presence or level of adipocytes in a cell or tissue sample. The antibodies can be used as an alternative means of treatment for obese patients other than undergoing surgery to remove excess fat. Antibodies for different types of fat deposits can also be produced e.g. intra-abdominal fat associated with heart disease
 Sequence 110 AA;
 Query Match 100.0%; Score 66; DB 4; Length 110;
 Best Local Similarity 100.0%; Pred. No. 0.0026;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 SGSTSNIGNNYVS 13
 |||||
 Db 23 SGSTSNIGNNYVS 35
 RESULT 5
 AAU02627

XX WPI; 2001-282031/29.
DR N-PSDB; AAS03451.
XX
PT Panel of specific binding members of antibody molecules which bind to
PT whole adipocytes is used in the treatment of obesity and obesity related
PT diseases.
XX
PS
XX
PS Claim 1; Page 124; 182pp; English.
XX
XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
CC and heavy chain complementarity determining regions (CDR) of the
CC invention. The antibodies can be used in the treatment of obesity and
CC obesity related diseases. The antibodies can be used to deliver drugs or
CC pro-drugs directly to the fat mass of an obese patient or the antibody
CC can be used as a therapeutic itself. Antibodies binding specifically to
CC adipocytes can be used to activate the immune system to destroy the cells
CC by complement mediated lysis. The antibodies may be labeled with a
CC detectable label such as radiolabel, fluorescent or chemical group and
CC used in methods of diagnosis in human subjects e.g. to determine the
CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease
XX
SQ Sequence 111 AA;

Query Match 100.0%; Score 66; DB 4; Length 111;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
| | | | | | | | | | | | | |
Db 24 SGSTSNIGNNYVS 36

RESULT 9
ABP45887
ID ABP45887 standard; protein; 240 AA.
XX
AC ABP45887;
XX
XX 19-AUG-2002 (first entry)
XX
DE Human BLYS binding scFv SEQ ID 1898.
XX
XX BLYS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
XX WO200202641-A1.
XX
XX 10-JAN-2002.
XX
XX 15-JUN-2001; 2001WO-US019110.
XX
XX 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
DR
XX
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1; Page 2666-2667; 3148pp; English.
XX
XX This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (BLYS) polypeptides. BLYS is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of BLYS. The antibodies bind to BLYS
CC and so may be used to detect and quantitate the presence of BLYS in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of BLYS. They may also be
CC administered to treat diseases associated with aberrant BLYS expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 240 AA;

Query Match 100.0%; Score 66; DB 5; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.0059;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
| | | | | | | | | | | | | |
Db 153 SGSTSNIGNNYVS 165

RESULT 10
ADG96714
ID ADG96714 standard; protein; 240 AA.
XX
AC ADG96714;
XX
XX 11-MAR-2004 (first entry)
XX
DE Single chain antibody that immunospecifically binds BLYS SeqID 1898.
XX
XX antibody; B lymphocyte stimulator; BLYS; tumour necrosis factor;
KW B cell proliferation; differentiation; scFv; myasthenia gravis;
KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KW carcinoma; lymphoma; antirheumatic; antiallergic; neuroprotective;
KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.
XX
OS Unidentified.
XX
XX WO2003055979-A2.
XX
XX 10-JUL-2003.
XX
XX 14-NOV-2002; 2002WO-US036496.
XX
XX 16-NOV-2001; 2001US-0331469P.
PR 19-DEC-2001; 2001US-0340817P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2003-505530/47.
XX
XX Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT (BLYS), useful for detecting and treating diseases or disorders e.g.

PT rheumatoid arthritis, asthma and leukemia.

XX Example 1; SEQ ID NO 1898; 394pp; English.

XX This invention relates to novel antibodies that immunospecifically bind

CC to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to

CC chromosome 13q34 and encodes a protein that is a member of the tumour

CC necrosis factor superfamily and induces both in vivo and in vitro B cell

CC proliferation and differentiation. Specifically, it refers to single

CC chain antibody molecules (scFvs) derived, preferably, from the variable

CC heavy CDR3 region that immunospecifically bind to a polypeptide, or

CC fragment thereof, of either human, murine, rat or monkey BLyS. The

CC present invention refers to the use of such antibodies in various methods

CC for the detection, diagnosis and prognosis of diseases related to the

CC aberrant expression or inappropriate function of BLyS or its receptor. As

CC such, these compositions are useful for identifying immune disorders

CC including myasthenia gravis and multiple sclerosis, inflammatory

CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such

CC as AIDS and proliferative disorders including leukaemia, carcinoma and

CC lymphoma. Accordingly, they can be described as exhibiting various

CC activities such as antirheumatic, antiarthritic, neuroprotective,

CC antiinflammatory, antiasthmatic, anti-allergic and cytostatic. This

CC polypeptide sequence is a single chain antibody that binds BLyS of the

CC invention. NOTE: The sequence data for this patent did not form part of

CC the printed specification, but was obtained in electronic format

CC directly from WIPO at ftp.wipo.int/pub/published pct_sequences.

XX

SQ Sequence 240 AA;

Query Match 100.0%; Score 66; DB 7; Length 240;

Best Local Similarity 100.0%; Pred. No. 0.0059;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13

Db 153 SGSTSNIGNNYVS 165

RESULT 11

ADG34301

ID ADG34301 standard; protein; 242 AA.

XX

AC ADG34301;

XX

XX 26-FEB-2004 (first entry)

XX Neurokinin B antibody SEQ ID NO:24.

XX antibody; neurokinin B; hypotensive; gynaecological; gene therapy;

XX hypertension; pre-eclampsia; NKB.

XX Synthetic.

XX WO2003102136-A2.

XX

PN 11-DEC-2003.

XX

XX 29-MAY-2003; 2003WO-US016802.

XX

XX 30-MAY-2002; 2002US-0383802P.

XX

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM;

XX

XX WPI; 2004-053456/05.

XX N-PSDB; ADG34282.

XX

XX New antibody that specifically binds neurokinin B, useful for preparing a

XX composition for treating or preventing hypertension or pre-eclampsia.

XX Claim 2; SEQ ID NO 24; 127pp; English.

CC The invention relates to a novel antibody specifically binding neurokinin

CC B. An antibody of the invention has hypotensive, and gynaecological

CC activity, and may have a use in gene therapy. The antibody is useful for

CC preparing a composition for treating or preventing hypertension or pre-

CC eclampsia. The present sequence is used in the exemplification of the

CC invention.

XX

SQ Sequence 242 AA;

Query Match 100.0%; Score 66; DB 8; Length 242;

Best Local Similarity 100.0%; Pred. No. 0.006;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13

Db 154 SGSTSNIGNNYVS 166

RESULT 12

ADG34317

ID ADG34317 standard; protein; 242 AA.

XX

AC ADG34317;

XX

XX 26-FEB-2004 (first entry)

XX Neurokinin B antibody SEQ ID NO:40.

XX

XX antibody; neurokinin B; hypotensive; gynaecological; gene therapy;

XX hypertension; pre-eclampsia; NKB.

XX Synthetic.

XX WO2003102136-A2.

XX

PN 11-DEC-2003.

XX

XX 29-MAY-2003; 2003WO-US016802.

XX

XX 30-MAY-2002; 2002US-0383802P.

XX

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM;

XX

XX WPI; 2004-053456/05.

XX N-PSDB; ADG34298.

XX

XX New antibody that specifically binds neurokinin B, useful for preparing a

XX composition for treating or preventing hypertension or pre-eclampsia.

XX Claim 2; SEQ ID NO 40; 127pp; English.

XX

XX The invention relates to a novel antibody specifically binding neurokinin

XX B. An antibody of the invention has hypotensive, and gynaecological

XX activity, and may have a use in gene therapy. The antibody is useful for

XX preparing a composition for treating or preventing hypertension or pre-

XX eclampsia. The present sequence is used in the exemplification of the

XX invention.

XX

SQ Sequence 242 AA;

Query Match 100.0%; Score 66; DB 8; Length 242;

Best Local Similarity 100.0%; Pred. No. 0.006;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13

Db 154 SGSTSNIGNNYVS 166

RESULT 13

ABP45916

```

ID ABP45916 standard; protein; 243 AA.
XX
AC ABP45916;
XX
DT 19-AUG-2002. (first entry)
XX
DE Human BlyS binding scFv SEQ ID 1927.
XX
KW BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
XX
PR 17-OCT-2000; 2000US-0240816P.
XX
PR 16-MAR-2001; 2001US-0276248P.
XX
PR 21-MAR-2001; 2001US-0277379P.
XX
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
XX
DR Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
XX diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1; Page 2700-2701; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte stimulator (BlyS) polypeptides. BlyS is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS
CC and so may be used to detect and quantitate the presence of BlyS in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of BlyS. They may also be
CC administered to treat diseases associated with aberrant BlyS expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 243 AA;
XX
Query Match 100.0%; Score 66; DB 5; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.006;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SGSTSNIIGNNYVS 13
Db 155 SGSTSNIIGNNYVS 167
RESULT 14
AAO31147
ID AAO31147 standard; protein; 243 AA.

```

```

XX
AC AAO31147;
XX
DT 06-OCT-2003 (first entry)
XX
DE Human CM085C11 scFv protein that specifically binds TR7.
XX
KW Human; protein coordinate data; heavy chain variable domain; VH; cancer;
KW complementarity determining region; CDR; light chain variable domain; VL;
KW TRAIL receptor 7; TR7; tumour necrosis factor; KILLER; death receptor 5;
KW DR5; TRAIL receptor 2; TRAIL-R2; TNF-related apoptosis-inducing ligand;
KW Kaposi's sarcoma; central nervous system; medulloblastoma; neuroblastoma;
KW glioblastoma; graft versus host disease; antibody therapy; neurotropic;
KW AIDS; acquired immune deficiency syndrome; neurodegenerative disorder;
KW immunosuppressive; neuroprotective; antibody therapy; antibody.
XX
OS Homo sapiens.
XX
PN WO2003054216-A2.
XX
PD 03-JUL-2003.
XX
PF 19-DEC-2002; 2002WO-US040597.
XX
PR 20-DEC-2001; 2001US-0341237P.
XX
PR 05-APR-2002; 2002US-0369877P.
XX
PR 04-JUN-2002; 2002US-0384828P.
XX
PR 18-JUL-2002; 2002US-0396591P.
XX
PR 15-AUG-2002; 2002US-0403370P.
XX
PR 13-NOV-2002; 2002US-0425737P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Salcedo T, Albert VR, Rosen CA, Humphreys R, Vaughan TJ;
XX WPI; 2003-569250/53.
XX
DR N-PSDB; AAL62844.
XX
PT New antibody or its fragment, useful for treating, preventing or
PT ameliorating a cancer, e.g. colon, breast, uterine, pancreatic, lung or
PT gastrointestinal cancer, or Kaposi's sarcoma or, graft versus host
XX disease, AIDS.
XX
PS Claim 2; Page 288; 301pp; English.
XX
CC The invention relates to an isolated antibody or its fragments such as
CC VHCDR1 (heavy chain variable domain complementarity determining region),
CC VHCDR2, VHCDR3, VLCDR1 (light chain variable domain complementarity
CC determining region), VLCDR2 or VLCDR3. The antibody or its fragment
CC immunospecifically binds TRAIL (tumour necrosis factor; TNF-related
CC apoptosis-inducing ligand) receptor 7 (TR7). TR7 is also referred to as
CC TRAIL receptor 2 (TRAIL-R2), death receptor 5 (DR5) and KILLER. The
CC antibody or its fragment is useful for treating, preventing or
CC ameliorating a cancer, e.g. colon, breast, uterine, pancreatic, lung or
CC gastrointestinal cancer or Kaposi's sarcoma or cancer of the central
CC nervous system such as medulloblastoma, neuroblastoma or glioblastoma or
CC graft versus host disease, AIDS (acquired immune deficiency syndrome) or
CC a neurodegenerative disorder. The invention is useful in antibody
CC therapy. The present sequence is human scFv protein that specifically
XX binds TR7
XX
SQ Sequence 243 AA;
XX
Query Match 100.0%; Score 66; DB 6; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.006;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SGSTSNIIGNNYVS 13
Db 155 SGSTSNIIGNNYVS 167
RESULT 15

```

Job time : 100.938 secs

ADG96743
ID ADG96743 standard; protein; 243 AA.
XX
XX AC ADG96743;
XX
XX DT 11-MAR-2004 (first entry)
XX
XX DE Single chain antibody that immunospecifically binds BlyS SeqID 1927.
XX
XX KW antibody; B lymphocyte stimulator; BlyS; tumour necrosis factor;
KW B cell proliferation; differentiation; scfv; myasthenia gravis;
KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KW carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.
XX
XX OS Unidentified.
XX
XX PN WO2003055979-A2.
XX
XX PD 10-JUL-2003.
XX
XX PF 14-NOV-2002; 2002WO-US036496.
XX
XX PR 16-NOV-2001; 2001US-0331469P.
XX
XX PR 19-DEC-2001; 2001US-0340817P.
XX
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
XX
XX DR WPI; 2003-505530/47.
XX
XX PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT (BlyS), useful for detecting and treating diseases or disorders e.g.
PT rheumatoid arthritis, asthma and leukemia.
XX
XX PS Example 1; SEQ ID NO 1927; 394pp; English.
XX
XX CC This invention relates to novel antibodies that immunospecifically bind
CC to B lymphocyte stimulator (BlyS). The BlyS gene has been mapped to
CC chromosome 13q34 and encodes a protein that is a member of the tumour
CC necrosis factor superfamily and induces both in vivo and in vitro B cell
CC proliferation and differentiation. Specifically, it refers to single
CC chain antibody molecules (scFvs) derived, preferably, from the variable
CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
CC fragment thereof, of either human, murine, rat or monkey BlyS. The
CC present invention refers to the use of such antibodies in various methods
CC for the detection, diagnosis and prognosis of diseases related to the
CC aberrant expression or inappropriate function of BlyS or its receptor. As
CC such, these compositions are useful for identifying immune disorders
CC including myasthenia gravis and multiple sclerosis, inflammatory
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC as AIDS and proliferative disorders including leukaemia, carcinoma and
CC lymphoma. Accordingly, they can be described as exhibiting various
CC activities such as antirheumatic, antiallergic, neuroprotective,
CC antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
CC polypeptide sequence is a single chain antibody that binds BlyS of the
CC invention. NOTE: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published pct_sequences.
XX
XX SQ Sequence 243 AA;
Query Match 100.0%; Score 66; DB 7; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.006;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
DB 155 SGSTSNIGNNYVS 167

Search completed: October 14, 2005, 16:12:41

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OM protein - protein search, using sw model

Run on: October 14, 2005, 16:00:04 ; Search time 25.5938 Seconds
(without alignments)
37.917 Million cell updates/sec

Title: US-10-614-959-13
Perfect score: 66
Sequence: 1 SGSTSNIGNNYVS 13

Scoring table: BLOSUM62
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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	62	93.9	98	2	US-08-665-202-37
3	62	93.9	98	4	US-09-315-574-37
4	62	93.9	111	2	US-08-665-202-36
5	62	93.9	111	2	US-08-665-202-42
6	62	93.9	111	2	US-08-665-202-43
7	62	93.9	111	3	US-08-983-607-35
8	62	93.9	111	4	US-09-315-574-36
9	62	93.9	111	4	US-09-315-574-42
10	62	93.9	111	4	US-09-315-574-43
11	62	93.9	112	2	US-08-665-202-39
12	62	93.9	112	3	US-08-983-607-31
13	62	93.9	112	3	US-09-025-769B-18
14	62	93.9	112	4	US-09-315-574-39
15	62	93.9	112	4	US-09-490-070A-18
16	62	93.9	112	4	US-09-490-153-18
17	62	93.9	112	4	US-09-490-324-18
18	62	93.9	114	3	US-09-240-274-62
19	62	93.9	234	4	US-09-372-425A-4
20	62	93.9	258	2	US-08-665-202-5
21	62	93.9	258	4	US-09-315-574-5
22	62	93.9	262	3	US-09-069-821-4
23	62	93.9	262	4	US-09-956-086-4
24	62	93.9	262	4	US-09-956-087-4
25	62	93.9	282	3	US-09-420-592A-7
26	62	93.9	282	4	US-09-985-442-7
27	62	93.9	282	4	US-09-983-580-7

ALIGNMENTS

RESULT 1

US-09-383-667-13

; Sequence 13, Application US/09383667

; Patent No. 6624295

; GENERAL INFORMATION:

; APPLICANT: Adams, Camelia W.

; APPLICANT: Devaux, Brigitte

; APPLICANT: Baton, Dan L.

; APPLICANT: Hass, Philip E.

; APPLICANT: Judice, J. Kevin

; APPLICANT: Kirchofer, Daniel

; APPLICANT: Suggett, Shelley

; TITLE OF INVENTION: Human Anti-Factor IX/Xa Antibodies

; FILE REFERENCE: P1661R2

; CURRENT APPLICATION NUMBER: US/09/383,667

; CURRENT FILING DATE: 1999-08-26

; EARLIER APPLICATION NUMBER: US 60/098,233

; EARLIER FILING DATE: 1998-08-28

; EARLIER APPLICATION NUMBER: US 60/122,767

; EARLIER FILING DATE: 1999-03-03

; NUMBER OF SEQ ID NOS: 32

; SEQ ID NO 13

; LENGTH: 13

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-383-667-13

Query Match

Best Local Similarity 100.0%; Score 66; DB 4; Length 13;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13

Db 1 SGSTSNIGNNYVS 13

RESULT 2

US-08-665-202-37

; Sequence 37, Application US/08665202

; Patent No. 5977322

; GENERAL INFORMATION:

; APPLICANT: Marks, James D.

; APPLICANT: Schler, Robert

; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to

; TITLE OF INVENTION: Tumor Antigens

; NUMBER OF SEQUENCES: 141

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

Sequence 15, Appl
Sequence 40, Appl
Sequence 40, Appl
Sequence 112, App
Sequence 32, Appl
Sequence 32, Appl
Sequence 51, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 51, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 51, Appl
Sequence 111, App
Sequence 38, Appl
Sequence 38, Appl
Sequence 59, Appl

/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/665,202
/ FILING DATE: 13-JUN-1996
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/000,238
/ FILING DATE: 14-JUN-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/000,250
/ FILING DATE: 15-JUN-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hunter, Tom
/ REGISTRATION NUMBER: 38,498
/ REFERENCE/DOCKET NUMBER: 02307E-061410
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 37:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 98 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-665-202-37

Query Match 93.9%; Score 62; DB 2; Length 98;
Best Local Similarity 92.3%; Pred. No. 0.007;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNVYS 13
|||:|||||||
Db 23 SGSSSNIGNNVYS 35

RESULT 3
US-09-315-574-37
/ Sequence 37, Application US/09315574
/ Patent No. 6512097
/ GENERAL INFORMATION:
/ APPLICANT: Marks, James D.
/ APPLICANT: Schlier, Robert
/ TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
/ Tumor Antigens
/ NUMBER OF SEQUENCES: 141
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
/ STREET: Four Embarcadero Center, Suite 1100
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-4106
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/315,574
/ FILING DATE: 20-MAY-99
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/000,238
/ FILING DATE: 14-JUN-1995
/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US 60/000,250
/ FILING DATE: 15-JUN-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/665,202
/ FILING DATE: 13-JUN-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hunter, Tom
/ REGISTRATION NUMBER: 38,498
/ REFERENCE/DOCKET NUMBER: 02307E-061411
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 37:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 98 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-09-315-574-37

Query Match 93.9%; Score 62; DB 4; Length 98;
Best Local Similarity 92.3%; Pred. No. 0.007;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNVYS 13
|||:|||||||
Db 23 SGSSSNIGNNVYS 35

RESULT 4
US-08-665-202-36
/ Sequence 36, Application US/08665202
/ Patent No. 5977322
/ GENERAL INFORMATION:
/ APPLICANT: Marks, James D.
/ APPLICANT: Schlier, Robert
/ TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
/ Tumor Antigens
/ NUMBER OF SEQUENCES: 141
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/665,202
/ FILING DATE: 13-JUN-1996
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/000,238
/ FILING DATE: 14-JUN-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/000,250
/ FILING DATE: 15-JUN-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hunter, Tom
/ REGISTRATION NUMBER: 38,498
/ REFERENCE/DOCKET NUMBER: 02307E-061410
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 36:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 111 amino acids
/ TYPE: amino acid

```

; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-665-202-36

Query Match          93.9%; Score 62; DB 2; Length 111;
Best Local Similarity 92.3%; Pred. No. 0.0079;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13
Db 23 SGSSSNIGNNYVS 35

RESULT 5
US-08-665-202-42
; Sequence 42, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061410
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-665-202-42

Query Match          93.9%; Score 62; DB 2; Length 111;
Best Local Similarity 92.3%; Pred. No. 0.0079;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13
Db 23 SGSSSNIGNNYVS 35

RESULT 6
US-08-665-202-43
; Sequence 43, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061410
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-665-202-43

Query Match          93.9%; Score 62; DB 2; Length 111;
Best Local Similarity 92.3%; Pred. No. 0.0079;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13
Db 23 SGSSSNIGNNYVS 35

RESULT 7
US-08-983-607-35
; Sequence 35, Application US/08983607
; Patent No. 6140470
; GENERAL INFORMATION:
; APPLICANT: Alan Garen
; APPLICANT: Xiaohong Cai
; TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
; TITLE OF INVENTION: bodies
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Department of Molecular Biophysics
; ADDRESSEE: and Biochemistry, Yale University
; STREET: 266 Whitney Avenue
; CITY: New Haven
; STATE: Connecticut
; COUNTRY: United States of America
; ZIP: 06520-8114
```

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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Word processing
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,607
FILING DATE: April 27, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB96/01032
FILING DATE: June 28, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mary M. Krinsky
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: OCR-679
TELEPHONE: 203-773-9544
TELEFAX: 203-773-1183
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: polypeptide
DESCRIPTION:
ORIGINAL SOURCE:
ORGANISM: Homo sapiens (melanoma patient immu-
INDIVIDUAL ISOLATE: peripheral blood lymphocytes
IMMEDIATE SOURCE:
LIBRARY: DM414 scFv antibodies obtained from
LIBRARY: FUSE5 fusion phage construct
CLONE: V373
FEATURE:
NAME/KEY: light chain
US-08-983-607-35

Query Match          93.9%; Score 62; DB 3; Length 111;
Best Local Similarity 92.3%; Pred. No. 0.0079;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13
   |||:|||||
Db 23 SGSSSNIGNNYVS 35

RESULT 8
US-09-315-574-36
; Sequence 36, Application US/09315574
; Patent No. 6512097
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
; STREET: Four Embarcadero Center, Suite 1100
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4106
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/315,574
; FILING DATE: 20-MAY-99
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/665,202
; FILING DATE: 13-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
```

```
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Word processing
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-315-574-36

Query Match          93.9%; Score 62; DB 4; Length 111;
Best Local Similarity 92.3%; Pred. No. 0.0079;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13
   |||:|||||
Db 23 SGSSSNIGNNYVS 35

RESULT 9
US-09-315-574-42
; Sequence 42, Application US/09315574
; Patent No. 6512097
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
; STREET: Four Embarcadero Center, Suite 1100
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4106
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/315,574
; FILING DATE: 20-MAY-99
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/665,202
; FILING DATE: 13-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
```



```

;
;   REGISTRATION NUMBER: 38,498
;   REFERENCE/DOCKET NUMBER: 02307E-061411
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 576-0200
;   TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 42:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 111 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   US-09-315-574-42

Query Match      93.9%; Score 62; DB 4; Length 111;
Best Local Similarity 92.3%; Pred. No. 0.0079;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SGSTSNIGNNYVS 13
      |||:|||||
Db      23 SGSSSNIGNNYVS 35

RESULT 10
US-09-315-574-43
; Sequence 43, Application US/09315574
; Patent No. 6512097
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
; STREET: Four Embarcadero Center, Suite 1100
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4106
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/315,574
; FILING DATE: 20-MAY-99
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061411
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-315-574-43

Query Match      93.9%; Score 62; DB 4; Length 111;
Best Local Similarity 92.3%; Pred. No. 0.0079;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SGSTSNIGNNYVS 13
      |||:|||||
Db      23 SGSSSNIGNNYVS 35

RESULT 11
US-08-665-202-39
; Sequence 39, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,202
; FILING DATE: 13-JUN-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061410
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-665-202-39

Query Match      93.9%; Score 62; DB 2; Length 112;
Best Local Similarity 92.3%; Pred. No. 0.008;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SGSTSNIGNNYVS 13
      |||:|||||
Db      23 SGSSSNIGNNYVS 35

RESULT 12
US-08-983-607-31
; Sequence 31, Application US/08983607
; Patent No. 6140470
; GENERAL INFORMATION:
; APPLICANT: Alan Garen
```

APPLICANT: Xiaohong Cai
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
bodies
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Department of Molecular Biophysics
ADDRESSEE: and Biochemistry, Yale University
STREET: 266 Whitney Avenue
CITY: New Haven
STATE: Connecticut
COUNTRY: United States of America
ZIP: 06520-8114
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Processing
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,607
FILING DATE: April 27, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB96/01032
FILING DATE: June 28, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mary M. Krinsky
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: OCR-679
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-773-9544
TELEFAX: 203-773-1183
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: polypeptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens (melanoma patient immu-
nized with autologous tumor cells)
INDIVIDUAL ISOLATE: peripheral blood lymphocytes
IMMEDIATE SOURCE:
LIBRARY: DM414 scFv antibodies obtained from
LIBRARY: FUSE5 fusion phage construct
CLONE: V73
FEATURE:
NAME/KEY: light chain
US-08-983-607-31
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Best Local Similarity 92.3%; Pred. No. 0.008;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SGSTSNIGNNVYS 13
Db 24 SGSSSNIGNNVYS 36
RESULT 13
US-09-025-769B-18
Sequence 18, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9090
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-18
Query Match 93.9%; Score 62; DB 3; Length 112;
Best Local Similarity 92.3%; Pred. No. 0.008;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SGSTSNIGNNVYS 13
Db 23 SGSSSNIGNNVYS 35
RESULT 14
US-09-315-574-39
Sequence 39, Application US/09315574
Patent No. 6512097
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
Tumor Antigens
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Haue P.C.
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-315-574-39

Query Match 93.9%; Score 62; DB 4; Length 112;
Best Local Similarity 92.3%; Pred. No. 0.008;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
Db 23 SGSSSNIGNNYVS 35

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Query Match 93.9%; Score 62; DB 4; Length 112;
Best Local Similarity 92.3%; Pred. No. 0.008;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 23 SGSSSNIGNNYVS 35

RESULT 15
US-09-490-070A-18
Sequence 18, Application US/094900070A
Patent No. 6696248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2005, 16:20:10 ; Search time 92.4219 Seconds
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Title: US-10-614-959-13
Perfect score: 66
Sequence: 1 SGSTSNIGNNYVS 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1859788 seqs, 416717961 residues

Total number of hits satisfying chosen parameters: 1859788

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA:**
- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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 - 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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 - 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
 - 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
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 - 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66	100.0	240	10	US-09-880-748-1898
2	66	100.0	240	15	Sequence 1898, Ap
3	66	100.0	242	18	Sequence 24, Appl
4	66	100.0	242	18	Sequence 40, Appl
5	66	100.0	243	10	US-09-880-748-1927
6	66	100.0	243	14	Sequence 1927, Ap
7	66	100.0	243	15	Sequence 53, Appl
8	66	100.0	243	18	Sequence 1927, Ap
9	66	100.0	243	18	Sequence 29, Appl
10	66	100.0	243	18	Sequence 33, Appl
11	66	100.0	243	18	Sequence 53, Appl

12	66	100.0	243	18	US-10-981-673-53
13	66	100.0	243	18	US-10-981-691-53
14	66	100.0	244	18	US-10-981-692-26
15	66	100.0	245	10	US-09-880-748-1926
16	66	100.0	245	15	US-10-293-418-1926
17	66	100.0	245	15	US-10-293-418-1926
18	66	100.0	245	18	US-10-981-692-31
19	66	100.0	245	18	US-10-981-692-36
20	66	100.0	246	10	US-09-880-748-1913
21	66	100.0	246	10	US-09-880-748-1917
22	66	100.0	246	15	US-10-293-418-1913
23	66	100.0	246	15	US-10-293-418-1917
24	66	100.0	247	10	US-09-880-748-1443
25	66	100.0	247	10	US-09-880-748-1682
26	66	100.0	247	10	US-09-880-748-1707
27	66	100.0	247	10	US-09-880-748-1899
28	66	100.0	247	10	US-09-880-748-1928
29	66	100.0	247	10	US-09-880-748-1934
30	66	100.0	247	15	US-10-293-418-1443
31	66	100.0	247	15	US-10-293-418-1682
32	66	100.0	247	15	US-10-293-418-1707
33	66	100.0	247	15	US-10-293-418-1899
34	66	100.0	247	15	US-10-293-418-1928
35	66	100.0	247	15	US-10-293-418-1934
36	66	100.0	247	17	US-10-935-290-46
37	66	100.0	247	17	US-10-935-290-88
38	66	100.0	247	18	US-10-981-692-27
39	66	100.0	247	18	US-10-981-692-37
40	66	100.0	247	20	US-11-046-857-44
41	66	100.0	248	18	US-10-981-692-39
42	66	100.0	249	10	US-09-880-748-1419
43	66	100.0	249	10	US-09-880-748-1618
44	66	100.0	249	10	US-09-880-748-2049
45	66	100.0	249	15	US-10-293-418-1419

ALIGNMENTS

RESULT 1
US-09-880-748-1898
; Sequence 1898, Application US/09880748
; Publication No. US20030055937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1898
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1898

Query Match 100.0%; Score 66; DB 10; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
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Db      153 SGSTSNIGNNYVS 165

RESULT 2
US-10-293-418-1898
; Sequence 1898, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1898
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1898

Query Match      100.0%; Score 66; DB 15; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SGSTSNIGNNYVS 13
Db      153 SGSTSNIGNNYVS 165

RESULT 3
US-10-981-692-24
; Sequence 24, Application US/10981692
; Publication No. US20050163777A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
; FILE REFERENCE: PF590P1
; CURRENT APPLICATION NUMBER: US/10/981,692
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: PCT/US03/16802
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/383,802
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Artificial sequence
; OTHER INFORMATION: N015E08 scFv
US-10-981-692-24

Query Match      100.0%; Score 66; DB 18; Length 242;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SGSTSNIGNNYVS 13
Db      153 SGSTSNIGNNYVS 165

RESULT 4
US-10-981-692-40
; Sequence 40, Application US/10981692
; Publication No. US20050163777A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
; FILE REFERENCE: PF590P1
; CURRENT APPLICATION NUMBER: US/10/981,692
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: PCT/US03/16802
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/383,802
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 76
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; SEQ ID NO 40
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: N015D10 scFv
US-10-981-692-40

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Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      154 SGSTSNIGNNYVS 166

RESULT 5
US-09-880-748-1927
; Sequence 1927, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1927
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1927

Query Match      100.0%; Score 66; DB 10; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SGSTSNIGNNYVS 13
Db      155 SGSTSNIGNNYVS 167
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; ORGANISM: Homo sapiens
US-10-293-418-1927

Query Match      100.0%; Score 66; DB 15; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SGSTSNIGNNYVS 13
DB      155 SGSTSNIGNNYVS 167

RESULT 8
US-10-981-692-29
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; Publication No. US20050163777A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
; FILE REFERENCE: PFS90P1
; CURRENT APPLICATION NUMBER: US/10/981,692
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: PCT/US03/16802
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/383,802
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; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: N024E07 scFv
US-10-981-692-29

Query Match      100.0%; Score 66; DB 18; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SGSTSNIGNNYVS 13
DB      155 SGSTSNIGNNYVS 167

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US-10-981-692-33
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; Publication No. US20050163777A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
; FILE REFERENCE: PFS90P1
; CURRENT APPLICATION NUMBER: US/10/981,692
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: PCT/US03/16802
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/383,802
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: N023E01 scFv
US-10-981-692-33

Query Match      100.0%; Score 66; DB 18; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SGSTSNIGNNYVS 13
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RESULT 6
US-10-322-673-53
; Sequence 53, Application US/10322673
; Publication No. US20030180296A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PFS85
; CURRENT APPLICATION NUMBER: US/10/322,673
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 72
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; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM085C11 scFv
US-10-322-673-53

Query Match      100.0%; Score 66; DB 14; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SGSTSNIGNNYVS 13
DB      155 SGSTSNIGNNYVS 167

RESULT 7
US-10-293-418-1927
; Sequence 1927, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1927
; LENGTH: 243
; TYPE: PRT
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Qy      1 SGSTSNIGNNYS 13
Db      155 SGSTSNIGNNYS 167

RESULT 10
US-10-981-465-53
; Sequence 53, Application US/10981465
; Publication No. US20050214205A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF585P1
; CURRENT APPLICATION NUMBER: US/10/981,465
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: 60/608,386
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: PCT/US04/013900
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: 60/468,092
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/495,140
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 10/322,673
; PRIOR FILING DATE: 2002-12-19
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; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
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; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: 60/468,092
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/495,140
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 10/322,673
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 76
; SEQ ID NO 53
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM085C11 scFv
US-10-981-465-53

Query Match      100.0%; Score 66; DB 18; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SGSTSNIGNNYS 13
Db      155 SGSTSNIGNNYS 167

RESULT 11
US-10-981-621-53
; Sequence 53, Application US/10981621
; Publication No. US20050214206A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF585P1D1
; CURRENT APPLICATION NUMBER: US/10/981,621
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: 60/608,386
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: PCT/US04/013900
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: 60/468,092
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/495,140
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; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 10/322,673
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 76
; SEQ ID NO 53
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM085C11 scFv
US-10-981-621-53

Query Match      100.0%; Score 66; DB 18; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SGSTSNIGNNYS 13
Db      155 SGSTSNIGNNYS 167

RESULT 12
US-10-981-673-53
; Sequence 53, Application US/10981673
; Publication No. US20050214207A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF585P1D2
; CURRENT APPLICATION NUMBER: US/10/981,673
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: 60/608,386
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: PCT/US04/013900
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: 60/468,092
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/495,140
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 10/322,673
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 76
; SEQ ID NO 53
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM085C11 scFv
US-10-981-673-53
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Query Match 100.0%; Score 66; DB 18; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.007; 0; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13
Db 155 SGSTSNIGNNYVS 167

RESULT 13
US-10-981-691-53
; Sequence 53, Application US/10981691
; Publication No. US20050214208A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF585PID3
; CURRENT APPLICATION NUMBER: US/10/981,691
; PRIOR FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: 60/608,386
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: PCT/US04/013900
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: 60/468,092
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/495,140
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 10/322,673
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 76
; SEQ ID NO 53
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CW085C11 scFv
US-10-981-691-53

Query Match 100.0%; Score 66; DB 18; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.007; 0; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13
Db 155 SGSTSNIGNNYVS 167

RESULT 14
US-10-981-692-26
; Sequence 26, Application US/10981692
; Publication No. US20050163777A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
; FILE REFERENCE: PF590P1
; CURRENT APPLICATION NUMBER: US/10/981,692
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: PCT/US03/16802
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/383,802
; PRIOR FILING DATE: 2002-05-30

; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: N024D01 scFv
US-10-981-692-26

Query Match 100.0%; Score 66; DB 18; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13
Db 156 SGSTSNIGNNYVS 168

RESULT 15
US-09-880-748-1926
; Sequence 1926, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1926
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1926

Query Match 100.0%; Score 66; DB 10; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13
Db 157 SGSTSNIGNNYVS 169

Search completed: October 14, 2005, 17:00:43
Job time : 92.4219 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2005, 16:02:59 ; Search time 18.0781 Seconds
(without alignments)
69.190 Million cell updates/sec

Title: US-10-614-959-13
Perfect score: 66
Sequence: 1 SGSTSNIGNNYVS 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: piri:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62	93.9	98	2 S36050	Ig lambda chain -
2	62	93.9	111	2 S47009	Ig lambda chain V1
3	62	93.9	111	2 S19664	Ig lambda chain V
4	62	93.9	113	2 A29700	Ig lambda chain V
5	62	93.9	232	2 S25742	Ig lambda chain -
6	62	93.9	235	2 S05270	Ig lambda chain -
7	59	89.4	130	2 S09712	Ig lambda chain V
8	57	86.4	130	1 L1HUBL	Ig lambda chain pr
9	56	84.8	111	2 S47185	Ig lambda chain -
10	56	84.8	131	2 S24321	Ig lambda chain -
11	55	83.3	111	1 L1HUNW	Ig lambda chain V-
12	53	80.3	98	2 S36048	Ig lambda chain -
13	53	80.3	111	1 L1HUNG	Ig lambda chain -
14	53	80.3	129	2 S78058	Ig lambda chain V-
15	53	80.3	130	2 S78057	Ig lambda chain pr
16	52	78.8	109	1 L1HUEP	Ig lambda chain V-
17	50	75.8	98	2 S36046	Ig lambda chain -
18	49	74.2	234	2 S25757	Ig lambda chain -
19	48	72.7	112	2 A44151	Ig lambda chain V
20	46	69.7	216	2 A42193	Ig lambda chain (B
21	45	68.2	98	2 S36047	Ig lambda chain -
22	45	68.2	110	2 S36258	Ig lambda chain V
23	45	68.2	112	2 D44151	Ig lambda chain V
24	45	68.2	117	2 S23627	Ig lambda chain pr
25	45	68.2	233	2 S25752	Ig lambda chain -
26	44	66.7	112	2 A44151	Ig lambda chain V
27	44	66.7	112	2 B44151	Ig lambda chain V
28	44	66.7	235	2 S25754	Ig lambda chain -
29	43.5	65.9	235	2 S14675	Ig lambda chain -

30	43	65.2	95	2 S49571	Ig lambda chain pr
31	43	65.2	149	2 S23626	Ig lambda chain V
32	43	65.2	2272	2 T18572	gag, pol and env p
33	43	65.2	2500	2 G71609	hypothetical prote
34	42	63.6	110	2 S57428	Ig light chain V-J
35	42	63.6	110	2 S57408	Ig lambda chain V-
36	42	63.6	233	2 S25744	Ig lambda chain -
37	42	63.6	348	2 F98997	uncharacterized co
38	41	62.1	99	2 S36054	Ig lambda chain -
39	41	62.1	107	2 B46516	Ig lambda chain V
40	41	62.1	111	1 L6HULT	Ig lambda chain V-
41	41	62.1	112	1 L1HUMM	Ig lambda chain V-
42	41	62.1	414	2 A71646	5-aminolevulinat
43	40	60.6	109	1 L1HUMA	Ig lambda chain V-
44	40	60.6	112	1 L1HUMA	Ig lambda chain V-
45	40	60.6	217	2 JE0246	Ig lambda chain NI

ALIGNMENTS

RESULT 1
S36050
Ig lambda chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C:Accession: S36050
R:Williams, S.C.
submitted to the EMBL Data Library, April 1993
A:Reference number: S36046
A:Accession: S36050
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-98 <WIL>
A:CROSS-references: EMBL:222191; NID:G312298; PIDN:CAA80201.1; PID:G312299
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-91/Domain: immunoglobulin homology <IMM>

Query Match 93.9%; Score 62; DB 2; Length 98;
Best Local Similarity 92.3%; Pred. No. 0.001;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
DB 23 SGSSNIGNNYVS 35
|||||

RESULT 2
S47009
Ig lambda chain V1-J3 region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C:Accession: S47009
R:Mahmoudi, M.; Gasyana, E.; Denomme, G.; Edwards, J.; Bell, D.; Cairns, E.
submitted to the EMBL Data Library, July 1994
A:Description: The role of the immunoglobulin heavy chain in human anti-DNA antibody bind
A:Reference number: S47009
A:Accession: S47009
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-111 <MAH>
A:CROSS-references: EMBL:235495; NID:G517346; PIDN:CAA84629.1; PID:G517347
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-91/Domain: immunoglobulin homology <IMM>

Query Match 93.9%; Score 62; DB 2; Length 111;
Best Local Similarity 92.3%; Pred. No. 0.0011;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
|||||

Db 23 SGSSSNIGNNYVS 35

RESULT 3

S19664

Ig lambda chain V region (clone alpha-phOx15) - human

C:Species: Homo sapiens (man)

C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000

C:Accession: S19664; S24444

R:Marka, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991

A:Title: By-passing immunization. Human antibodies from V-gene libraries displayed on phage

A:Reference number: S19663; MUID:92085276; PMID:1748994

A:Accession: S19664

A:Molecule type: mRNA

A:Residues: 1-111 <MAR>

A:Cross-references: EMBL:X61641

R:Jones, P.T.

submitted to the EMBL Data Library, October 1991

A:Reference number: S24442

A:Accession: S24444

A:Molecule type: mRNA

A:Residues: 1-110, 'W' <JON>

A:Cross-references: EMBL:X61641; NID:g35458; PIDN:CAA43822.1; PID:g1335271

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-91/Domain: immunoglobulin homology <IMM>

Query Match 93.9%; Score 62; DB 2; Length 111;

Best Local Similarity 92.3%; Pred. No. 0.0011; Indels 0; Gaps 0;

Matches 12; Conservative 1; Mismatches 0;

Qy 1 SGSTSNIGNNYVS 13

Db 23 SGSSSNIGNNYVS 35

RESULT 4

A29700

Ig lambda chain V region (Zim) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 21-Jan-2000

C:Accession: A29700

R:Eulitz, M.; Breuer, M.; Linke, R.P.

Biol. Chem. Hoppe-Seyler 368, 863-870, 1987

A:Title: Is the formation of AL-type amyloid promoted by structural peculiarities of immunoglobulin V region?

A:Reference number: A29700; MUID:87299022; PMID:3620114

A:Accession: A29700

A:Molecule type: protein

A:Residues: 1-113 <EUL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:14-90/Domain: immunoglobulin homology <IMM>

Query Match 93.9%; Score 62; DB 2; Length 113;

Best Local Similarity 92.3%; Pred. No. 0.0012; Indels 0; Gaps 0;

Matches 12; Conservative 1; Mismatches 0;

Qy 1 SGSTSNIGNNYVS 13

Db 22 SGSSSNIGNNYVS 34

RESULT 5

S25742

Ig lambda chain - human

C:Species: Homo sapiens (man)

C>Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S25742

R:Combratio, G.; Klobeck, H.G.

Eur. J. Immunol. 21, 1513-1522, 1991

A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lambda chain

A:Reference number: S16439; MUID:91257162; PMID:1904362

A:Accession: S25742

A>Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-232 <COM>

A:Cross-references: EMBL:X57806; NID:g33709; PIDN:CAA40944.1; PID:g33710

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:147-215/Domain: immunoglobulin homology <IMM>

Query Match 93.9%; Score 62; DB 2; Length 232;

Best Local Similarity 92.3%; Pred. No. 0.0025; Indels 0; Gaps 0;

Matches 12; Conservative 1; Mismatches 0;

Qy 1 SGSTSNIGNNYVS 13

Db 39 SGSSSNIGNNYVS 51

RESULT 6

S05270

Ig lambda chain precursor - human

C:Species: Homo sapiens (man)

C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000

C:Accession: S05270; S04601

R:Kishimoto, T.

submitted to the EMBL Data Library, March 1989

A:Reference number: S05270

A:Accession: S05270

A:Molecule type: mRNA

A:Residues: 1-235 <KIS1>

A:Cross-references: EMBL:X14583; NID:g33394; PIDN:CAA32725.1; PID:g33395

R:Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.

Nucleic Acids Res. 17, 4385, 1989

A:Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of immunoglobulin lambda chain precursor

A:Reference number: S04601; MUID:89296497; PMID:2500644

A:Accession: S04601

A:Molecule type: mRNA

A:Residues: 1-130 <KIS2>

A:Cross-references: EMBL:X14583

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-235/Product: Ig lambda chain #status predicted <MAT>

F:150-218/Domain: immunoglobulin homology <IMM>

Query Match 93.9%; Score 62; DB 2; Length 235;

Best Local Similarity 92.3%; Pred. No. 0.0025; Indels 0; Gaps 0;

Matches 12; Conservative 1; Mismatches 0;

Qy 1 SGSTSNIGNNYVS 13

Db 42 SGSSSNIGNNYVS 54

RESULT 7

S09712

Ig lambda chain V region - human

C:Species: Homo sapiens (man)

C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C:Accession: S09712

R:Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.

Biochem. J. 268, 135-140, 1990

A:Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains of immunoglobulin lambda chain V region

A:Reference number: S09710; MUID:90262535; PMID:2111699

A:Accession: S09712

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-130 <HUG>

A:Cross-references: GB:X52109; NID:g31454; PIDN:CAA36343.1; PID:g31455

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-110/Domain: immunoglobulin homology <IMM>

```
Query Match      89.4%; Score 59; DB 2; Length 130;
Best Local Similarity 84.6%; Pred. No. 0.0045;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGTSTNIGNNYVS 13
Db 42 SGTSSNIGNNYVS 54

RESULT 8
LIHUBL
Ig lambda chain precursor V-I region (BL2) - human
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C:Accession: A01966
R:Tsujiimoto, Y.; Croce, C.M.
Nucleic Acids Res. 12, 8407-8414, 1984
A:Title: Molecular cloning of a human immunoglobulin lambda chain variable sequence.
A:Reference number: A01966; MUID:85062823; PMID:6095199
A:Accession: A01966
A:Molecule type: mRNA
A:Residues: 1-130 <TSU>
A:Cross-references: UNIPROT:P06316; GB:X01147; NID:G33335; PIDN:CAA25598.1; PID:g758087
C:Genetics:
A:Gene: GDB:IGLV@
A:Cross-references: GDB:119342; OMIM:147240
A:Map position: 22q11.2-22q11.2
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-130/Product: Ig lambda chain V-I region (BL2) #status predicted <MAT>
F:20-115/Region: V segment
F:34-110/Domain: immunoglobulin homology <IMM>
F:116-130/Region: J segment
F:41-108/Disulfide bonds: #status predicted

Query Match      86.4%; Score 57; DB 1; Length 130;
Best Local Similarity 84.6%; Pred. No. 0.01;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGTSTNIGNNYVS 13
Db 42 SGTSSNIGNNYVS 54

RESULT 9
S47185
Ig lambda chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S47185
F:McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.
submitted to the EMBL Data Library, June 1994
A:Description: Cloning and analysis of IGM anti-thyroglobulin autoantibodies from patien
A:Reference number: S47181
A:Accession: S47185
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-111 <MCI>
A:Cross-references: NID:G506428; PIDN:CAA56178.1; PID:G506429
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-90/Domain: immunoglobulin homology <IMM>

Query Match      84.8%; Score 56; DB 2; Length 111;
Best Local Similarity 84.6%; Pred. No. 0.013;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SGTSTNIGNNYVS 13
Db 22 SGTSSNIGNNYVS 34
```

```
RESULT 10
S24321
Ig lambda chain precursor - human
C:Species: Homo sapiens (man)
C>Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S24321
R:Aucouturier, P.; Khamlichi, A.A.; Preud'homme, J.L.; Bauwens, M.; Touchard, G.; Cogné,
Biochem. J. 285, 149-152, 1992
A:Title: Complementary DNA sequence of human amyloidogenic immunoglobulin light-chain pr
A:Reference number: S24319; MUID:92344562; PMID:1379039
A:Accession: S24321
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-131 <AUC>
A:Cross-references: EMBL:X64134; NID:G32808; PIDN:CAA45495.1; PID:G32809
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-110/Domain: immunoglobulin homology <IMM>

Query Match      84.8%; Score 56; DB 2; Length 131;
Best Local Similarity 84.6%; Pred. No. 0.015;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SGTSTNIGNNYVS 13
Db 42 SGTSSNIGNNYVS 54

RESULT 11
LIHUNW
Ig lambda chain V-I region (New) - human
C:Species: Homo sapiens (man)
C>Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C:Accession: A01964
R:Langer, B.; Steinmetz-Kayne, M.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 349, 945-951, 1968
A:Title: The complete amino acid sequence of Bence-Jones protein New (lambda type) . Subg
A:Reference number: A01964; MUID:69060892; PMID:4177823
A:Accession: A01964
A:Molecule type: protein
A:Residues: 1-111 <LAN>
A:Cross-references: UNIPROT:P01701
C:Comment: This is a Bence Jones protein.
C:Genetics:
A:Gene: GDB:IGLV@
A:Cross-references: GDB:119342; OMIM:147240
A:Map position: 22q11.2-22q11.2
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: blocked amino end; heterotetramer
F:15-91/Domain: immunoglobulin homology <IMM>
F:1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #statu
F:22-89/Disulfide bonds: #status predicted

Query Match      83.3%; Score 55; DB 1; Length 111;
Best Local Similarity 76.9%; Pred. No. 0.019;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SGTSTNIGNNYVS 13
Db 23 SGTSTNIGNNYVS 35

RESULT 12
S36048
Ig lambda chain - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C:Accession: S36048; S36049
R:Williams, S.C.
```

```
submitted to the EMBL Data Library, April 1993
A;Reference number: S36046
A;Accession: S36048
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <WU>
A;Cross-references: EMBL:Z22189; NID:g312294; PIDN:CAA80199.1; PID:g312295; EMBL:Z22190
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-91/Domain: immunoglobulin homology <IMM>

Query Match      80.3%; Score 53; DB 2; Length 98;
Best Local Similarity 83.3%; Pred. No. 0.037;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYV 12
   |||:||||:|
Db 23 SGSSSNIQSNV 34

RESULT 13
LIHUNG
Ig lambda chain V-I region (Nig-64) - human (tentative sequence)
C;Species: Homo sapiens (man)
C;Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004
C;Accession: A01965
R;Kametani, F.; Takayasu, T.; Suzuki, S.; Shinoda, T.; Okuyama, T.; Shimizu, A.
J. Biochem. 93, 421-429, 1983
A;Title: Comparative studies on the structure of the light chains of human immunoglobulin
A;Reference number: A91970; MUID:83186114; PMID:6404900
A;Accession: A01965
A;Molecule type: protein
A;Residues: 1-111 <KAW>
A;Cross-references: UNIPROT:P01702
C;Genetics:
A;Gene: GDB:IGLV@
A;Cross-references: GDB:119342; OMIM:147240
A;Map position: 22q11.2-22q11.2
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap)
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: blocked amino end; heterotetramer
F;15-91/Domain: immunoglobulin homology <IMM>
F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #statu
F;22-89/Disulfide bonds: #status predicted

Query Match      80.3%; Score 53; DB 1; Length 111;
Best Local Similarity 76.9%; Pred. No. 0.042;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
   |||:||||:|
Db 23 SGSSSNIQDNFVS 35

RESULT 14
S78058
Ig lambda chain precursor V-J region (clone mAb 67VL) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C;Accession: S78058; S23723
R;Harindranath, N.
submitted to the EMBL Data Library, August 1990
A;Reference number: S78051
A;Accession: S78058
A;Molecule type: mRNA
A;Residues: 1-129 <HAR>
A;Cross-references: EMBL:X54446; NID:g37923; PIDN:CAA38313.1; PID:g930121
R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins
Int. Immunol. 3, 865-875, 1991
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
patient.
A;Reference number: S23716; MUID:92031262; PMID:1718404

Query Match      80.3%; Score 53; DB 2; Length 130;
Best Local Similarity 83.3%; Pred. No. 0.049;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYV 12
   |||:||||:|
Db 42 SGSSSNIQSNV 53

Search completed: October 14, 2005, 16:23:38
Job time : 18.0781 secs
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```
A;Accession: S23723
A;Molecule type: mRNA
A;Residues: 19-129 <HAW>
A;Cross-references: EMBL:X54446
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-18/Domain: signal sequence (fragment) #status predicted <SIG>
F;19-129/Product: Ig lambda chain (fragment) #status predicted <MAT>
F;33-109/Domain: immunoglobulin homology <IMM>

Query Match      80.3%; Score 53; DB 2; Length 129;
Best Local Similarity 83.3%; Pred. No. 0.049;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYV 12
   |||:||||:|
Db 41 SGSSSNIQSNV 52

RESULT 15
S78057
Ig lambda chain precursor V-J region (clone mAb 61VL) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C;Accession: S78057; S23722
R;Harindranath, N.
submitted to the EMBL Data Library, August 1990
A;Reference number: S78051
A;Accession: S78057
A;Molecule type: mRNA
A;Residues: 1-130 <HAR>
A;Cross-references: EMBL:X54438; NID:g37920; PIDN:CAA38307.1; PID:g37921
R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins,
Int. Immunol. 3, 865-875, 1991
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
patient.
A;Reference number: S23716; MUID:92031262; PMID:1718404
A;Accession: S23722
A;Molecule type: mRNA
A;Residues: 20-130 <HAW>
A;Cross-references: EMBL:X54438
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-130/Product: Ig lambda chain (fragment) #status predicted <MAT>
F;34-110/Domain: immunoglobulin homology <IMM>

Query Match      80.3%; Score 53; DB 2; Length 130;
Best Local Similarity 83.3%; Pred. No. 0.049;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYV 12
   |||:||||:|
Db 42 SGSSSNIQSNV 53

Search completed: October 14, 2005, 16:23:38
Job time : 18.0781 secs
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OM protein - protein search, using sw model

Run on: October 14, 2005, 15:51:44 ; Search time 86.5312 Seconds
(without alignments)
76.932 Million cell updates/sec

Title: US-10-614-959-13
Perfect score: 66
Sequence: 1 SGSTSNIGNNVYS 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	57	86.4	130	1	LV1G_HUMAN	P06316 homo sapien
2	56	84.8	101	2	Q81ZD8	Q81ZD8 homo sapien
3	55	83.3	110	2	Q8TE63	Q8TE63 homo sapien
4	55	83.3	111	1	LV1C_HUMAN	P01701 homo sapien
5	53	80.3	108	2	Q96S80	Q96S80 homo sapien
6	53	80.3	111	1	LV1D_HUMAN	P01702 homo sapien
7	52	78.8	109	1	LV1I_HUMAN	P06888 homo sapien
8	52	78.8	235	2	Q6IN99	Q6IN99 homo sapien
9	51	77.3	236	2	Q8NEJ1	Q8NEJ1 homo sapien
10	49	74.2	237	2	Q6DHW4	Q6DHW4 homo sapien
11	45	68.2	235	2	Q6GMW6	Q6GMW6 homo sapien
12	44	66.7	221	2	Q87LH3	Q87LH3 vibrio para
13	44	66.7	326	2	Q7SCJ5	Q7SCJ5 neurospora
14	44	66.7	441	2	Q8JRX2	Q8JRX2 phthorimaea
15	43	65.2	1170	2	Q7WZ9N	Q7WZ9N pseudomonas
16	43	65.2	1357	2	Q9W4M4	Q9W4M4 drosophila
17	43	65.2	2186	1	YL52_CAEEL	P34431 caenorhabdi
18	43	65.2	2272	2	Q17329	Q17329 caenorhabdi
19	43	65.2	2500	2	Q96223	Q96223 plasmodium
20	42	63.6	236	2	Q6GMV7	Q6GMV7 homo sapien
21	42	63.6	348	2	Q97KX3	Q97KX3 clostridium
22	42	63.6	633	1	ACES_ELEEL	Q62775 electrophor
23	41	62.1	111	1	LV6D_HUMAN	P06318 homo sapien
24	41	62.1	112	1	LV1H_HUMAN	P06887 homo sapien
25	41	62.1	388	2	Q9VRW7	Q9VRW7 drosophila
26	41	62.1	414	1	HEM1_RICPR	Q92C8B rickettsia
27	41	62.1	414	2	Q68V53	Q68V53 rickettsia
28	41	62.1	847	2	Q6BK59	Q6BK59 debaryomyce
29	41	62.1	958	2	Q7RR78	Q7RR78 plasmodium
30	41	62.1	1272	2	Q95S84	Q95S84 drosophila
31	41	62.1	1272	2	Q9W117	Q9W117 drosophila

ALIGNMENTS

RESULT 1

LV1G_HUMAN	STANDARD;	PRT;	130 AA.
AC P06316;			
DT 01-JAN-1988 (Rel. 06, Created)			
DT 01-JAN-1988 (Rel. 06, Last sequence update)			
DT 15-JUL-1999 (Rel. 38, Last annotation update)			
DE Ig lambda chain V-I region BL2 precursor.			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX NCBI_TaxID=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=85062823; PubMed=6095199;			
RA Tsujimoto Y., Croce C.M.;			
RT "Molecular cloning of a human immunoglobulin lambda chain variable			
RT sequence".			
RL Nucleic Acids Res. 12:8407-8414(1984).			
CC -----			
CC This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -			
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CC use by non-profit institutions as long as its content is in no way			
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CC or send an email to license@isb-sib.ch).			
CC -----			
DR EMBL; X01147; CAA25598.1; -			
DR PIR; A01966; L1HUBL.			
DR HSPF; P01703; 7FAB.			
DR GO; GO:0005576; C:extracellular; NAS.			
DR GO; GO:0003823; F:antigen binding; NAS.			
DR GO; GO:0006955; P:immune response; NAS.			
DR InterPro; IPR007110; Ig-like.			
DR InterPro; IPR003596; Ig_v.			
DR Pfam; PF00047; Ig; 1.			
DR SMART; SM00406; IGV; 1.			
DR PROSITE; PS50835; IG LIKE; 1.			
KW Immunoglobulin V region; Signal.			
FT SIGNAL 1 19			
FT CHAIN 20 130			Ig lambda chain V-I region BL2.
FT DOMAIN 20 115			V segment.
FT DOMAIN 116 130			J segment.
FT DISULFID 41 108			By similarity.
FT NON TER 130 130			
SQ SEQUENCE 130 AA; 13564 MW; FA44BB17D3A55EBF CRC64;			

Query Match 86.4%; Score 57; DB 1; Length 130;
Best Local Similarity 84.6%; Pred. No. 0.069;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNVYS 13

|||||:||||

Db 42 SGSSSNGNDYVS 54

RESULT 2

Q81ZD8
ID Q81ZD8 PRELIMINARY; PRT; 101 AA.
AC Q81ZD8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-thyroglobulin light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Jang Y.-J., Chung J., Park J.-Y.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY145444; AAN64328.1; -.
DR HSP; P01703; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 101
FT NON_TER 101 101
SQ SEQUENCE 101 AA; 10374 MW; 1506C2D9AACBA793 CRC64;

Query Match 84.8%; Score 56; DB 2; Length 101;
Best Local Similarity 84.6%; Pred. No. 0.079;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SGSTSNGNNTVS 13

Db 13 SGSSSNGKNYVS 25

RESULT 3

Q8TE63
ID Q8TE63 PRELIMINARY; PRT; 110 AA.
AC Q8TE63;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Immunoglobulin light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=95007525; PubMed=7923137;
RA Hall B.L., Murray J.H., Haspel M.V., Kobrin B.J.;
RT "Establishment, molecular rescue, and expression of 123AV16-1, a
RT tumor-reactive human monoclonal antibody.";
RL Cancer Res. 54:5178-5185(1994).
DR EMBL; L33985; AAL68704.1; -.
DR HSP; P01703; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 110
FT NON_TER <1 >110 immunoglobulin light chain variable
FT CHAIN region.
FT NON_TER 110 110
FT NON_TER 110 AA; 11479 MW; 599D1628F8F5437C CRC64;
SQ SEQUENCE 110 AA; 11479 MW; 599D1628F8F5437C CRC64;

Query Match 83.3%; Score 55; DB 2; Length 110;

Best Local Similarity 76.9%; Pred. No. 0.13;

Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNGNNYVS 13
Db 23 SGTSSNGNFVS 35

RESULT 4

LV1C_HUMAN
ID LV1C_HUMAN STANDARD; PRT; 111 AA.
AC P01701;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 03-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda chain V-I region NEW.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=69060892; PubMed=4177823;
RA Langer B., Steinmetz-Kayne M., Hilschmann N.;
RT "The complete amino acid sequence of Bence Jones protein New (lambda-
RT type). Subgroups in the variable part of immunoglobulin L-chains of
RL the lambda-type.";
RL Hoppe-Seyler's Z. Physiol. Chem. 349:945-951(1968).
CC -|- MISCELLANEOUS: This is a Bence-Jones protein.
CC -|- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01964; LIHUNW.
DR HSP; P01703; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT DOMAIN 1 105
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT DISULFID 22 89 By similarity.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11453 MW; AAECBCA3C49F2AD3 CRC64;

Query Match 83.3%; Score 55; DB 1; Length 111;
Best Local Similarity 76.9%; Pred. No. 0.13;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SGSTSNGNNYVS 13

Db 23 SGTSSNGNNYVS 35

RESULT 5

Q96SB0
ID Q96SB0 PRELIMINARY; PRT; 108 AA.
AC Q96SB0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-streptococcal/anti-mycosin immunoglobulin lambda light chain
DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98375893; PubMed=9712075;
RA Aderson E.B., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-mycosin


```
RT antibody V region genes."
RL J. Immunol. 161:2020-2031(1998).
DR EMBL, U96394; AAB68783.1; -.
DR FDB; 1KU4; Model; L=1-108.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON TER 1
SQ SEQUENCE 108 AA; 11594 MW; F4B5DC478A043F48 CRC64;

Query Match      80.3%; Score 53; DB 2; Length 108;
Best Local Similarity 83.3%; Pred. No. 0.28;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGSTSNIGNNYV 12
DB 23 SGSSSNIGSNYV 34

RESULT 6
LV1D_HUMAN
ID LV1D_HUMAN STANDARD; PRT; 111 AA.
AC P01702;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda chain V-I region NIG-64.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=8186114; PubMed=6404900;
RA Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
RA Shimizu A.;
RT "Comparative studies on the structure of the light chains of human
RT immunoglobulins. IV. Assignment of a subgroup."
J. Biochem. 93:421-429(1983).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01965; LIHUEP.
DR HSSP; P01703; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region;
KW Pyrolydione carboxylic acid.
FT DOMAIN 1 105
FT MOD RES 1 1 Pyrolydione carboxylic acid.
FT DISULFID 22 89 By similarity.
FT NON TER 111 111
SQ SEQUENCE 111 AA; 11454 MW; A21C612C18A61E0 CRC64;

Query Match      80.3%; Score 53; DB 1; Length 111;
Best Local Similarity 76.9%; Pred. No. 0.29;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGSTSNIGNNYVS 13
DB 23 SGSSSNIGDNFVS 35

RESULT 7
LV1I_HUMAN
ID LV1I_HUMAN STANDARD; PRT; 109 AA.
AC P06880;
DT 01-JAN-1988 (Rel. 06, Created)
DR EMBL, U96394; AAB68783.1; -.
DR FDB; 1KU4; Model; L=1-108.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON TER 1
SQ SEQUENCE 108 AA; 11594 MW; F4B5DC478A043F48 CRC64;

Query Match      80.3%; Score 52; DB 1; Length 109;
Best Local Similarity 83.3%; Pred. No. 0.42;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 SGSTSNIGNNYV 12
DB 23 SGSSSNIGKNYV 34

RESULT 8
O6IN99
ID O6IN99 PRELIMINARY; PRT; 235 AA.
AC O6IN99;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGLC2 protein.
GN Name=IGLC2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RX Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bheh F.,
RX Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RX Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RX Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RX Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RX Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RX Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RX Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RX Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Pancreas;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC072392; AAH7392.1; -.
DR HSSP; P01842; IAAK.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 235 AA; 24888 MW; 90C95D5B97A6BCC1 CRC64;

Query Match 78.8%; Score 52; DB 2; Length 235;
Best Local Similarity 76.9%; Pred. No. 0.9;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNVYS 13
Db ||:||||:||||
42 SGRSSNIGNSYVS 54

RESULT 9
Q8NEJ1 ID Q8NEJ1 PRELIMINARY; PRT; 236 AA.
AC Q8NEJ1
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC075843; AAH75843.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
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RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC030984; AAH30984.1; -.
DR HSSP; P01703; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25024 MW; 1703B77942630E08 CRC64;

Query Match 77.3%; Score 51; DB 2; Length 236;
Best Local Similarity 83.3%; Pred. No. 1.3;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNVY 12
Db |||:||||:||||
42 SGRSSNIGNSYV 53

RESULT 10
Q6DHW4 ID Q6DHW4 PRELIMINARY; PRT; 237 AA.
AC Q6DHW4
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC075843; AAH75843.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
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DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IgC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS08335; IG LIKE; 2.
DR PROSITE; PS08335; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein_1.
SQ SEQUENCE 237 AA; 25108 MW; 6814170F7E784825 CRC64;

Query Match      74.2%; Score 49; DB 2; Length 237;
Best Local Similarity 83.3%; Pred. No. 3;
Matches 10; Conservative 1; Mismatches 0; Gaps 0;

QY 1 SGSTSNIGNNYV 12
DB 42 SGSSSNGIGNYV 53

RESULT 11
O6GMW6 PRELIMINARY; PRT; 235 AA.
AC O6GMW6;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussid T.B., Toshlyuk S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073784; AAH73784.1; -
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.

us-10-614-959-13.rup
DR PROSITE; PS08335; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 24803 MW; 05805F61118F1B8 CRC64;

Query Match      68.2%; Score 45; DB 2; Length 235;
Best Local Similarity 69.2%; Pred. No. 14;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
DB 42 SGSSSNGIGNSVN 54

RESULT 12
Q87LH3 PRELIMINARY; PRT; 221 AA.
AC Q87LH3;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Putative short-chain dehydrogenase.
GN OrderedLocusNames=VP2639;
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najiima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";
RL Lancet 361:743-749 (2003).
DR EMBL; AP005082; BAC6902.1; -
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002198; ADH short.
DR InterPro; IPR002347; Adh_short_C2.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00081; GDHRDH.
DR Complete proteome.
SQ SEQUENCE 221 AA; 23803 MW; D545E953C9AB3A2F CRC64;

Query Match      66.7%; Score 44; DB 2; Length 221;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GSTSNIGNNYVS 13
DB 203 GALANIGNYVS 214

RESULT 13
Q7SCJ5 PRELIMINARY; PRT; 326 AA.
AC Q7SCJ5;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=NCU00836.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,

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RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M., Schulte U.,
RA Selftreinikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Greenberg D.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Gnerre S.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamvassellis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmari S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbola D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.,
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AABX01000101; EAA34466.1; -.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro: IPR00254; CBD fungal.
DR InterPro: IPR005103; Glyco_hydro_61.
DR Pfam: PF00734; CBM.1; 1.
DR Pfam: PF03443; Glyco_hydro_61; 1.
DR PROSITE: PS00562; CBD_FUNGAL; 1.
KW Hypothetical protein.
SQ SEQUENCE 326 AA; 33269 MW; 61BC539A292B959F CRC64;

Query Match 66.7%; Score 44; DB 2; Length 326;
Best Local Similarity 61.5%; Pred. No. 30;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13
Db 311 SGSTCKVGNDDYS 323

RESULT 14
Q8JRX2 PRELIMINARY; PRT; 441 AA.
AC Q8JRX2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Late expression factor 4.
GN Name=PhopGV087;
OS Phthorimaea operculella granulovirus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
OC NCBI_TaxID=192584;
RN [1]
RP SEQUENCE FROM N.A.
RA Croizier L., Taha A., Croizier G., Lopez Ferber M.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF499596; AAM70285.1; -.
DR GO: GO:0030528; P:transcription regulator activity; IEA.
DR GO: GO:0045449; P:regulation of transcription; IEA.
DR InterPro: IPR007790; LEF-4.
DR Pfam: PF05098; LEF-4; 1.
SQ SEQUENCE 441 AA; 51639 MW; DC7B3982323E3550 CRC64;

Query Match 66.7%; Score 44; DB 2; Length 441;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYV 12
Db 264 SGNLFNIGNNYL 275

RESULT 15
Q7WZN9

ID Q7WZN9 PRELIMINARY; PRT; 1170 AA.
AC Q7WZN9;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DT Pili1.
GN Name=piliY1;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PA14;
RX PubMed=14983043; DOI=10.1073/pnas.0304622101;
RA He J., Baldini R.L., Dexiel E., Saucier M., Zhang Q., Liberati N.T.,
RA Lee D., Urbach J., Goodman H.M., Rahme L.G.;
RT "The broad host range pathogen Pseudomonas aeruginosa strain PA14
RT carries two pathogenicity islands harboring plant and animal virulence
RT genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2530-2535(2004).
RL EMBL: AY273871; AAP81276.1; -.
DR InterPro: IPR008707; Neisseria_pilc.
DR Pfam: PF05567; Neisseria_PilC; 1.
SQ SEQUENCE 1170 AA; 128118 MW; 9F4CDF6D681B62F3 CRC64;
Query Match 65.2%; Score 43; DB 2; Length 1170;
Best Local Similarity 70.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GSTSNIGNNY 11
Db 139 GSTTNSNNY 148

Search completed: October 14, 2005, 16:19:55
Job time : 88.5312 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2005, 15:51:19 ; Search time 53.8125 Seconds
(without alignments)
50.310 Million cell updates/sec

Title: US-10-614-959-14
Perfect score: 35
Sequence: 1 DVSKRPS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:.*
1: Genesecp1980s:.*
2: Genesecp1990s:.*
3: Genesecp2000s:.*
4: Genesecp2001s:.*
5: Genesecp2002s:.*
6: Genesecp2003as:.*
7: Genesecp2003bs:.*
8: Genesecp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	7	3 AAY79072	Aay79072 Anti-fact
2	35	100.0	99	7 ADJ80338	Adj80338 Vlamda g
3	35	100.0	109	4 AAU02544	Aau02544 Anti-adip
4	35	100.0	110	3 AAY96060	Aay96060 Human ant
5	35	100.0	110	4 AAU02558	Aau02558 Anti-adip
6	35	100.0	110	4 AAU02612	Aau02612 Anti-adip
7	35	100.0	110	4 AAU02627	Aau02627 Anti-adip
8	35	100.0	110	4 AAU02629	Aau02629 Anti-adip
9	35	100.0	111	2 AAU19883	Aau19883 CEA-speci
10	35	100.0	111	4 AAU02542	Aau02542 Anti-adip
11	35	100.0	111	4 AAU02551	Aau02551 Anti-adip
12	35	100.0	111	4 AAU02585	Aau02585 Anti-adip
13	35	100.0	111	7 ADK17416	Adk17416 Anti-huma
14	35	100.0	111	8 ADG42838	Adg42838 scFv Ab12
15	35	100.0	214	8 ABM85072	Abm85072 Human dia
16	35	100.0	236	8 ABM85084	Abm85084 Human dia
17	35	100.0	240	5 ABP45887	Abp45887 Human Bly
18	35	100.0	240	7 ADG96714	Adg96714 Single ch
19	35	100.0	241	5 ABP46044	Abp46044 Human Bly
20	35	100.0	241	7 ADG96871	Adg96871 Single ch
21	35	100.0	242	8 ADG34301	Adg34301 Neurokini
22	35	100.0	242	8 ADG34317	Adg34317 Neurokini
23	35	100.0	243	5 ABP45916	Abp45916 Human Bly
24	35	100.0	243	7 ADG96743	Adg96743 Single ch
25	35	100.0	243	8 ADG34310	Adg34310 Neurokini

26	35	100.0	243	8 ADG34306	Adg34306 Neurokini
27	35	100.0	244	8 ADG34303	Adg34303 Neurokini
28	35	100.0	245	5 ABP45915	Abp45915 Human Bly
29	35	100.0	245	7 ADG96742	Adg96742 Single ch
30	35	100.0	245	7 ADG98057	Adg98057 TNF proli
31	35	100.0	245	8 ADE83862	Ade83862 Chemokine
32	35	100.0	245	8 ADG34308	Adg34308 Neurokini
33	35	100.0	245	8 ADG34313	Adg34313 Neurokini
34	35	100.0	246	5 ABP45902	Abp45902 Human Bly
35	35	100.0	246	5 ABP45906	Abp45906 Human Bly
36	35	100.0	246	7 ADG96733	Adg96733 Single ch
37	35	100.0	246	7 ADG96729	Adg96729 Single ch
38	35	100.0	246	8 AD883872	Ad883872 Chemokine
39	35	100.0	247	5 ABP45671	Abp45671 Human Bly
40	35	100.0	247	5 ABP45674	Abp45674 Human Bly
41	35	100.0	247	5 ABP45432	Abp45432 Human Bly
42	35	100.0	247	5 ABP45923	Abp45923 Human Bly
43	35	100.0	247	5 ABP45917	Abp45917 Human Bly
44	35	100.0	247	5 ABP45696	Abp45696 Human Bly
45	35	100.0	247	5 ABP45888	Abp45888 Human Bly

ALIGNMENTS

RESULT 1
AAY79072

ID AAY79072 standard; peptide; 7 AA.

XX AAY79072;

XX DT 12-JUN-2000 (first entry)

XX DE Anti-factor IX/IXa antibody L chain V domain CDR2 amino acid sequence.
KW Complementarity determining region 2; CDR2; antibody; Gla domain;
KW factor IX/IXa, blood coagulation; deep venous thrombosis; light chain;
KW arterial thrombosis; unstable angina; post myocardial infarction;
KW coronary artery bypass graft; CABG; stroke; tumour growth; metastasis;
KW percutaneous transluminal coronary angioplasty; PTCA; inflammation;
KW septic shock; hypotension; adult respiratory distress syndrome; ARDS;
KW arterial fibrillation; disseminated intravascular coagulopathy; DIC.

OS Homo sapiens.

XX WO200012562-A1.

XX PD 09-MAR-2000.

XX PF 26-AUG-1999; 99WO-US019453.

XX PR 28-AUG-1998; 98US-0098233P.

XX PR 03-MAR-1999; 99US-0122767P.

XX (GETH) GENENTECH INC.

XX PI Adams CW, Devaux B, Eaton DL, Haas PE, Judice JK, Kirchhofer D;
XX Suggett S;

XX WPI; 2000-256595/22.

XX PT Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-
XX carboxyglutamic acid domains useful as anti-coagulant in thrombosis,
XX stroke, and post myocardial infarction.

XX PS Claim 8; Fig 2; 84pp; English.

XX CC This sequence represents a complementarity determining region 2 (CDR2) of
XX the light chain variable domain of a human anti-factor IX/IXa Gla domain
XX antibody. Factor IXa is a vitamin K dependent plasma serine protease that
XX participates in the blood coagulation pathways. The Gla domain of factor
XX IXa and its zymogen factor IX contains important structural determinants
XX for interaction with high affinity binding sites on vascular endothelial

CC cells and platelets. Compositions comprising the antibodies are used for
CC the treatment or prophylaxis of thrombotic or coagulopathic diseases or
CC disorders in a mammal for which inhibiting a FIX/IXa mediated event is
CC indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable
CC angina, post myocardial infarction, post surgical thrombosis, coronary
CC artery bypass graft (CABG), percutaneous transluminal coronary
CC angioplasty (PTCA), stroke, tumor growth, invasion or metastasis,
CC inflammation, septic shock, hypotension, adult respiratory distress
CC syndrome (ARDS), arterial fibrillation and disseminated intravascular
CC coagulopathy (DIC)
XX
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 35; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
| | | | |
Db 1 DVSKRPS 7

RESULT 2

ADJ80338
ID ADJ80338 standard; protein; 99 AA.

XX
AC ADJ80338;

XX
DT 06-MAY-2004 (first entry)

XX
DE Vlamda gene locus antibody amino acid sequence #7.

XX
KW hybrid antibody; antibody; framework region; homology; immunogenicity.

XX
OS Homo sapiens.

XX
PN WO2003048321-A2.

XX
PD 12-JUN-2003.

XX
PF 03-DEC-2002; 2002WO-US038450.

XX
PR 03-DEC-2001; 2001US-0336591P.

XX
PA (ALEX-) ALEXTON PHARM INC.

XX
PI Rother R, Wu D;

XX
XX WPI; 2003-513753/48.

XX
PT Producing a hybrid antibody or hybrid antibody fragment by operatively
PT linking the selected framework sequences to one or more complementarity
PT determining regions of the initial antibody.

XX
PS Disclosure; SEQ ID NO 98; 77pp; English.

XX The invention relates to a method of producing a hybrid antibody or
CC hybrid antibody fragment by: (i) providing an initial antibody having
CC specificity for a target; (ii) determining the sequence of a variable
CC region of the initial antibody; (iii) selecting a first component of the
CC variable region consisting of FR1, FR2, FR3 and FR4; (iv) comparing the
CC sequence of the first component to sequences contained in a reference
CC database of antibody sequences or antibody fragment sequences from a
CC target species; (v) selecting a sequence from an antibody in the database
CC which demonstrates a high degree of homology to the first component; (vi)
CC selecting a second component of the variable region which is different
CC than the first component, the second component selected from the group
CC consisting of FR1, FR2, FR3 and FR4; (vii) comparing the sequence of the
CC second component to sequences contained in a reference database of the
CC antibody sequences or antibody fragment sequences from the target species
CC; (viii) selecting a sequence from the database which demonstrates a high
CC degree of homology to the second component and which is from a different
CC antibody than the selected antibody; and (ix) operatively linking the

CC selected framework sequences to one or more complementarity determining
CC regions (CDRs) of the initial antibody to produce a hybrid antibody or
CC hybrid antibody fragment. The method is useful for producing a hybrid
CC antibody or hybrid antibody fragment (claimed). The antibody and
CC fragments are useful for therapeutic and diagnostic purposes. The method
CC uses entire framework regions from a single antibody variable heavy or
CC variable light chain to receive the CDRs. This produces antibodies that
CC are highly homologous and exhibit reduced immunogenicity while
CC maintaining an optimum binding profile. This sequence represents the
CC amino acid sequence of an antibody from the Vlamda gene locus.

XX
SQ Sequence 99 AA;

Query Match 100.0%; Score 35; DB 7; Length 99;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
| | | | |
Db 52 DVSKRPS 58

RESULT 3

AAU02544

ID AAU02544 standard; protein; 109 AA.

XX
AC AAU02544;

XX
DT 29-AUG-2001 (first entry)

XX
DE Anti-adipocyte monoclonal antibody light chain, FAT 31.

XX
KW Antibody; adipocyte; heavy chain; light chain; obesity; fat;
KW heart disease; complementarity determining region; CDR.

XX
OS Homo sapiens.

XX
PN WO200127279-A1.

XX
PD 19-APR-2001.

XX
PF 11-OCT-2000; 2000WO-GB003900.

XX
PR 12-OCT-1999; 99US-0158812P.

XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX
PI Edwards BM, Main SH, Vaughan TJ;

XX
DR WPI; 2001-282031/29.

XX
DR N-PSDB; AAS0344.

XX
PT Panel of specific binding members of antibody molecules which bind to
PT whole adipocytes is used in the treatment of obesity and obesity related
PT diseases.

XX
PS Claim 1; Page 120; 182pp; English.

XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
CC and heavy chain complementarity determining regions (CDR) of the
CC invention. The antibodies can be used in the treatment of obesity and
CC obesity related diseases. The antibodies can be used to deliver drugs or
CC pro-drugs directly to the fat mass of an obese patient or the antibody
CC can be used as a therapeutic itself. Antibodies binding specifically to
CC adipocytes can be used to activate the immune system to destroy the cells
CC by complement mediated lysis. The antibodies may be labeled with a
CC detectable label such as radiolabel, fluorescent or chemical group and
CC used in methods of diagnosis in human subjects e.g. to determine the
CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies

CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease
XX
SQ Sequence 109 AA;

Query Match 100.0%; Score 35; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 51 DVSKRPS 57
|||||

RESULT 4
AA96060
ID AAY96060 standard; protein; 110 AA.
XX
AC AAY96060;
XX
DT 05-DEC-2000 (first entry)
XX
DE Human anti-DAP antibody LU30 light chain variable region.
XX
KW LU30; human; antibody; VL domain; decay accelerating factor; DAF;
KW phage display; subtractive panning; lung cancer; lung carcinoma;
KW lung adenocarcinoma; therapy; diagnosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH Region 23..36
FT /label= CDRI
FT /note= "complementarity determining region I"
FT Region 25..35
FT /note= "hypervariable loop region"
FT Region 52..58
FT /label= CDRII
FT /note= "complementarity determining region II"
FT Region 52..54
FT /note= "hypervariable loop residues"
FT Region 91..100
FT /label= CDRIII
FT /note= "complementarity determining region III"
FT Region 93..99
FT /note= "hypervariable loop residues"
XX
DN WO200052054-A2.
XX
PD 08-SEP-2000.
XX
PF 29-FEB-2000; 2000WO-US005352.
XX
PR 01-MAR-1999; 99US-0122262P.
XX
PA (GETH) GENENTECH INC.
XX
PI Carter PJ, Ridgway JB;
XX
DR WPI; 2000-594169/56.
XX
XX
XX Making antibodies (e.g. anti-decay accelerating factor antibody) for
XX diagnosing or treating e.g. lung cancer comprises identifying an antigen
XX that is differentially expressed on the surface of two or more distinct
XX cell populations.
XX
PS Disclosure; Fig 5A; 52pp; English.
XX
XX
XX The present sequence is that of the light chain variable region (VL) of
XX the anti-decay accelerating factor (DAF) human antibody LU30. The VH
XX region is given in AAY06063. LU30 has a binding affinity (Kd) for DAF of
XX about 13 nM. It was produced using a novel method for making antibodies
XX which can be used for cancer diagnosis or therapy. The method comprises:

CC (a) binding an antibody phage from a naive antibody phage library to a
CC live cancer cell; (b) selecting an antibody phage or antibody which binds
CC selectively to the live cancer cell; and (c) identifying an antigen to
CC which the antibody phage or antibody binds. To obtain LU30, a human scFv
CC library was used to search for tumour-associated antigens by panning the
CC lung adenocarcinoma cell line 1264, and counter-selecting with a non-
CC tumour bronchial epithelial cell line, BEAS-2B. The invention also
CC describes a method for identifying an antigen which is differentially
CC expressed on the surface of 2 or more distinct cell populations. The anti-
CC -DAF human antibody, or a composition comprising the antibody, is useful
CC for in vivo cancer diagnosis or therapy. In particular, the antibody is
CC useful for diagnosing or treating lung cancer, e.g. small-cell lung
CC cancer, non-small cell lung cancer, large cell lung carcinoma, lung
CC adenocarcinoma, or squamous cell lung carcinoma (all claimed)
XX
SQ Sequence 110 AA;

Query Match 100.0%; Score 35; DB 3; Length 110;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 52 DVSKRPS 58
|||||

RESULT 5
AAU02558
ID AAU02558 standard; protein; 110 AA.
XX
AC AAU02558;
XX
DT 29-AUG-2001 (first entry)
XX
DE Anti-adipocyte monoclonal antibody light chain, FAT 44.
XX
KW Antibody; adipocyte; heavy chain; light chain; obesity; fat;
KW heart disease; complementarity determining region; CDR.
XX
OS Homo sapiens.
XX
PN WO200127279-A1.
XX
PD 19-APR-2001.
XX
PF 11-OCT-2000; 2000WO-GB003900.
XX
PR 12-OCT-1999; 99US-0158812P.
XX
PA (CMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Edwards BM, Main SH, Vaughan TJ;
XX
DR WPI; 2001-282031/29.
XX
DR N-PSDB; AAS03458.
XX
XX Panel of specific binding members of antibody molecules which bind to
XX whole adipocytes is used in the treatment of obesity and obesity related
XX diseases.
XX
XX Claim 1; Page 128-129; 182pp; English.
XX
XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
XX sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
XX and heavy chain complementarity determining regions (CDR) of the
XX invention. The antibodies can be used in the treatment of obesity and
XX obesity related diseases. The antibodies can be used to deliver drugs or
XX pro-drugs directly to the fat mass of an obese patient or the antibody
XX can be used as a therapeutic itself. Antibodies binding specifically to
XX adipocytes can be used to activate the immune system to destroy the cells
XX by complement mediated lysis. The antibodies may be labeled with a
XX detectable label such as radiolabel, fluorescent or chemical group and
XX used in methods of diagnosis in human subjects e.g. to determine the

CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease
XX
XX Sequence 110 AA;

Query Match 100.0%; Score 35; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 51 DVSKRPS 57

RESULT 6

AAU02612
ID AAU02612 standard; protein; 110 AA.

XX AAU02612;

DT 29-AUG-2001 (first entry)

XX Anti-adipocyte monoclonal antibody light chain, FAT 99.

DE Antibody; adipocyte; heavy chain; light chain; obesity; fat;
KW heart disease; complementarity determining region; CDR.

XX Homo sapiens.

XX WO200127279-A1.

XX 19-APR-2001.

XX 11-OCT-2000; 2000WO-GB003900.

XX 12-OCT-1999; 99US-0158812P.

XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Edwards BM, Main SH, Vaughan TJ;

XX WPI; 2001-282031/29.

XX N-PSDB; AAS03512.

XX Panel of specific binding members of antibody molecules which bind to
XX whole adipocytes is used in the treatment of obesity and obesity related
XX diseases.

XX Claim 1; Page 163; 182pp; English.

XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
XX sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
XX and heavy chain complementarity determining regions (CDR) of the
XX invention. The antibodies can be used in the treatment of obesity and
XX obesity related diseases. The antibodies can be used to deliver drugs or
XX pro-drugs directly to the fat mass of an obese patient or the antibody
XX can be used as a therapeutic itself. Antibodies binding specifically to
XX adipocytes can be used to activate the immune system to destroy the cells
XX by complement mediated lysis. The antibodies may be labeled with a
XX detectable label such as radiolabel, fluorescent or chemical group and
XX used in methods of diagnosis in human subjects e.g. to determine the
XX presence of adipocyte antigen on the surface of an adipocyte to detect or
XX determine the presence or level of adipocytes in a cell or tissue sample.
XX The antibodies can be used as an alternative means of treatment for obese
XX patients other than undergoing surgery to remove excess fat. Antibodies
XX for different types of fat deposits can also be produced e.g. intra-
XX abdominal fat associated with heart disease

XX Sequence 110 AA;

Query Match 100.0%; Score 35; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 51 DVSKRPS 57

RESULT 7

AAU02627
ID AAU02627 standard; protein; 110 AA.

XX AAU02627;

DT 29-AUG-2001 (first entry)

XX Anti-adipocyte monoclonal antibody light chain, FAT 112.

DE Antibody; adipocyte; heavy chain; light chain; obesity; fat;
KW heart disease; complementarity determining region; CDR.

XX Homo sapiens.

XX WO200127279-A1.

XX 19-APR-2001.

XX 11-OCT-2000; 2000WO-GB003900.

XX 12-OCT-1999; 99US-0158812P.

XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Edwards BM, Main SH, Vaughan TJ;

XX WPI; 2001-282031/29.

XX N-PSDB; AAS03527.

XX Panel of specific binding members of antibody molecules which bind to
XX whole adipocytes is used in the treatment of obesity and obesity related
XX diseases.

XX Claim 1; Page 172; 182pp; English.

XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
XX sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
XX and heavy chain complementarity determining regions (CDR) of the
XX invention. The antibodies can be used in the treatment of obesity and
XX obesity related diseases. The antibodies can be used to deliver drugs or
XX pro-drugs directly to the fat mass of an obese patient or the antibody
XX can be used as a therapeutic itself. Antibodies binding specifically to
XX adipocytes can be used to activate the immune system to destroy the cells
XX by complement mediated lysis. The antibodies may be labeled with a
XX detectable label such as radiolabel, fluorescent or chemical group and
XX used in methods of diagnosis in human subjects e.g. to determine the
XX presence of adipocyte antigen on the surface of an adipocyte to detect or
XX determine the presence or level of adipocytes in a cell or tissue sample.
XX The antibodies can be used as an alternative means of treatment for obese
XX patients other than undergoing surgery to remove excess fat. Antibodies
XX for different types of fat deposits can also be produced e.g. intra-
XX abdominal fat associated with heart disease

XX Sequence 110 AA;

Query Match 100.0%; Score 35; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 51 DVSKRPS 57

RESULT 8
AAU02629
ID .AAU02629 standard; protein; 110 AA.
XX AC AAU02629;
XX
XX 29-AUG-2001 (first entry)
XX
XX Anti-adipocyte monoclonal antibody light chain, FAT 113.
XX DE
XX Antbody; adipocyte; heavy chain; light chain; obesity; fat;
KW heart disease; complementarity determining region; CDR.
XX OS
XX Homo sapiens.
XX PN WO200127279-A1.
XX PD 19-APR-2001.
XX 11-OCT-2000; 2000WO-GB003900.
XX PF 12-OCT-1999; 99US-0158812P.
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX Edwards BM, Main SH, Vaughan TJ;
XX WPI; 2001-282031/29.
XX DR N-PSDB; AAS03529.
XX
XX Panel of specific binding members of antibody molecules which bind to
PT whole adipocytes is used in the treatment of obesity and obesity related
PT diseases.
XX
XX Claim 1; Page 173; 182pp; English.
XX
XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
CC and heavy chain complementarity determining regions (CDR) of the
CC invention. The antibodies can be used in the treatment of obesity and
CC obesity related diseases. The antibodies can be used to deliver drugs or
CC pro-drugs directly to the fat mass of an obese patient or the antibody
CC can be used as a therapeutic itself. Antibodies binding specifically to
CC adipocytes can be used to activate the immune system to destroy the cells
CC by complement mediated lysis. The antibodies may be labeled with a
CC detectable label such as radiolabel, fluorescent or chemical group and
CC used in methods of diagnosis in human subjects e.g. to determine the
CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease
XX
XX Sequence 110 AA;
XX
Query Match 100.0%; Score 35; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 DVSKRPS 7
Db 51 DVSKRPS 57
RESULT 9
AAU19883
ID AAU19883 standard; protein; 111 AA.
XX AC AAU19883;
XX

07-DEC-1997 (first entry)
CEA-specific antibody CEAl, CEAl2, CEAl3 VL sequence.
Carcinoembryonic antigen; CEA; human; antibody; scFv; tumour marker;
lung cancer; breast cancer; colon cancer; adenocarcinoma; diagnosis.
Homo sapiens.
Key Location/Qualifiers
Region 23..35
/label= CDR1
/note= "complementarity determining region 1"
Region 50..56
/label= CDR2
/note= "complementarity determining region 2"
Region 90..100
/label= CDR3
/note= "complementarity determining region 3"
WO9720932-A1.
12-JUN-1997.
09-DEC-1996; 96WO-GB003043.
07-DEC-1995; 95GB-00025004.
23-MAY-1996; 96GB-00010824.
11-OCT-1996; 96GB-00021295.
(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
Osbourne JK, Allen DJ, McCafferty JG;
WPI; 1997-319779/29.
N-PSDB; AAT72133.
Specific binding members for human carcinoembryonic antigen - bind to the
A3-B3 extracellular domain of hCEA and are substantially non-cross-
reactive with human liver cells; used for diagnosing cancer.
Claim 14; Fig 1b; 128pp; English.
This polypeptide sequence comprises the light chain variable region (VL)
of human carcinoembryonic antigen (hCEA)-specific antibodies CEAl, CEAl2
and CEAl3. VH (AAT72126-32) and VL (AAT72133-35) gene sequences were
obtained for anti-hCEA antibodies CEAl-CEA7 (see AAW19876-85). A claimed
specific binding member (A) comprises an hCEA specific antibody antigen
binding domain that has a dissociation constant for hCEA of less than 1 x
10⁻⁸ M, is non-cross-reactive with human liver cells, and
preferentially binds to the A3-B3 extracellular domain of hCEA and/or to
cell-associated hCEA over hCEA over soluble hCEA. Preferred (A) include
pairings of VH and VL sequences from CEAl-7, or their CDR sequences, as
well as CEAl6 VH and VL variants. (A) is used to detect cells expressing
hCEA, in vivo or in vitro, especiallyly tumour cells for diagnosing cancer,
e.g. adenocarcinoma of the colon, lung or breast

Query Match 100.0%; Score 35; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 DVSKRPS 7
Db 51 DVSKRPS 57
RESULT 10
AAU02542
ID AAU02542 standard; protein; 111 AA.
XX AC AAU02542;

```
XX 29-AUG-2001 (first entry)
DT
XX
XX Anti-adipocyte monoclonal antibody light chain, FAT 30.
DE
XX
XX Antibody; adipocyte; heavy chain; light chain; obesity; fat;
KW heart disease; complementarity determining region; CDR.
XX
XX Homo sapiens.
OS
XX WO200127279-A1.
PN
XX
XX 19-APR-2001.
PD
XX
XX 11-OCT-2000; 2000WO-GB003900.
PF
XX
XX 12-OCT-1999; 99US-0158812P.
PR
XX
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PA
XX
XX Edwards BM, Main SH, Vaughan TJ;
PI
XX
XX WPI; 2001-282031/29.
DR
XX
XX N-PSDB; AAS03442.
DR
XX
XX Panel of specific binding members of antibody molecules which bind to
PT whole adipocytes is used in the treatment of obesity and obesity related
PT diseases.
PT
XX
XX Claim 1; Page 118-119; 182pp; English.
PS
XX
XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
CC and heavy chain complementarity determining regions (CDR) of the
CC invention. The antibodies can be used in the treatment of obesity and
CC obesity related diseases. The antibodies can be used to deliver drugs or
CC pro-drugs directly to the fat mass of an obese patient or the antibody
CC can be used as a therapeutic itself. Antibodies binding specifically to
CC adipocytes can be used to activate the immune system to destroy the cells
CC by complement mediated lysis. The antibodies may be labeled with a
CC detectable label such as radiolabel, fluorescent or chemical group and
CC used in methods of diagnosis in human subjects e.g. to determine the
CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease
XX
XX SQ Sequence 111 AA;
XX
XX Query Match 100.0%; Score 35; DB 4; Length 111;
XX Best Local Similarity 100.0%; Pred. No. 6.1;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 DVSKRPS 7
XX |||||
XX 51 DVSKRPS 57
XX
XX DB
XX
XX RESULT 11
XX AAU02551
XX ID AAU02551 standard; protein; 111 AA.
XX
XX AC AAU02551;
XX
XX 29-AUG-2001 (first entry)
XX
XX Anti-adipocyte monoclonal antibody light chain, FAT 37.
DE
XX
XX Antibody; adipocyte; heavy chain; light chain; obesity; fat;
KW heart disease; complementarity determining region; CDR.
XX
XX
```

```
OS Homo sapiens.
XX WO200127279-A1.
PN
XX
XX 19-APR-2001.
PD
XX
XX 11-OCT-2000; 2000WO-GB003900.
PF
XX
XX 12-OCT-1999; 99US-0158812P.
PR
XX
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PA
XX
XX Edwards BM, Main SH, Vaughan TJ;
PI
XX
XX WPI; 2001-282031/29.
DR
XX
XX N-PSDB; AAS03451.
DR
XX
XX Panel of specific binding members of antibody molecules which bind to
PT whole adipocytes is used in the treatment of obesity and obesity related
PT diseases.
PT
XX
XX Claim 1; Page 124; 182pp; English.
PS
XX
XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
CC and heavy chain complementarity determining regions (CDR) of the
CC invention. The antibodies can be used in the treatment of obesity and
CC obesity related diseases. The antibodies can be used to deliver drugs or
CC pro-drugs directly to the fat mass of an obese patient or the antibody
CC can be used as a therapeutic itself. Antibodies binding specifically to
CC adipocytes can be used to activate the immune system to destroy the cells
CC by complement mediated lysis. The antibodies may be labeled with a
CC detectable label such as radiolabel, fluorescent or chemical group and
CC used in methods of diagnosis in human subjects e.g. to determine the
CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease
XX
XX SQ Sequence 111 AA;
XX
XX Query Match 100.0%; Score 35; DB 4; Length 111;
XX Best Local Similarity 100.0%; Pred. No. 6.1;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 DVSKRPS 7
XX |||||
XX 52 DVSKRPS 58
XX
XX DB
XX
XX RESULT 12
XX AAU02585
XX ID AAU02585 standard; protein; 111 AA.
XX
XX AC AAU02585;
XX
XX 29-AUG-2001 (first entry)
XX
XX Anti-adipocyte monoclonal antibody light chain, FAT 72.
DE
XX
XX Antibody; adipocyte; heavy chain; light chain; obesity; fat;
KW heart disease; complementarity determining region; CDR.
XX
XX OS Homo sapiens.
XX
XX WO200127279-A1.
PN
XX
XX 19-APR-2001.
PD
XX
XX 11-OCT-2000; 2000WO-GB003900.
PF
XX
XX
```

PR 12-OCT-1999; 99US-0158812P.
 XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PA Edwards BM, Main SH, Vaughan TJ;
 XX WPI; 2001-282031/29.
 XX DR N-PSDB; AAS03485.
 XX Panel of specific binding members of antibody molecules which bind to
 PT whole adipocytes is used in the treatment of obesity and obesity related
 PT diseases.
 XX Claim 1; Page 146; 182pp; English.
 XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
 CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
 CC and heavy chain complementarity determining regions (CDR) of the
 CC invention. The antibodies can be used in the treatment of obesity and
 CC obesity related diseases. The antibodies can be used to deliver drugs or
 CC pro-drugs directly to the fat mass of an obese patient or the antibody
 CC can be used as a therapeutic itself. Antibodies binding specifically to
 CC adipocytes can be used to activate the immune system to destroy the cells
 CC by complement mediated lysis. The antibodies may be labeled with a
 CC detectable label such as radiolabel, fluorescent or chemical group and
 CC used in methods of diagnosis in human subjects e.g. to determine the
 CC presence of adipocyte antigen on the surface of an adipocyte to detect or
 CC determine the presence or level of adipocytes in a cell or tissue sample.
 CC The antibodies can be used as an alternative means of treatment for obese
 CC patients other than undergoing surgery to remove excess fat. Antibodies
 CC for different types of fat deposits can also be produced e.g. intra-
 CC abdominal fat associated with heart disease
 XX Sequence 111 AA;
 SQ Query Match 100.0%; Score 35; DB 4; Length 111;
 Best Local Similarity 100.0%; Pred. No. 6.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DVSKRPS 7
 DB 51 DVSKRPS 57
 RESULT 13
 ADK17416
 ID ADK17416 standard; protein; 111 AA.
 XX AC ADK17416;
 XX 06-MAY-2004 (first entry)
 DT Anti-human CXCR4 loop 6 ScFv antibody V1 region.
 DE anti-HIV; cytostatic; virucide; single chain antibody; antibody; yeast;
 KW HIV; cancer; CCR5.
 KW Synthetic.
 XX WO2003066830-A2.
 XX 14-AUG-2003.
 PD 07-FEB-2003; 2003WO-US003763.
 PF 08-FEB-2002; 2002US-00071866.
 PR 08-FEB-2002; 2002US-00072031.
 PR 25-APR-2002; 2002US-00133978.
 XX (GENE-) GENETASTIX CORP.
 PA Hua S, Pauling MH, Zhu L;
 PI WPI; 2004-051479/05.
 XX

DR WPI; 2003-731501/69.
 XX Selecting an scFv against a peptide target by expressing a target fusion
 PT protein having a DNA binding domain or activation domain of a
 PT transcription activator, useful for diagnosing, preventing and/or
 PT treating HIV infection and cancer.
 XX Claim 123; SEQ ID NO 61; 150pp; English.
 XX The invention relates to a method of selecting a single chain antibody
 CC (scFv) against a peptide target in a yeast by expressing a library of
 CC scFv fusion proteins in yeast cells, expressing a target fusion protein
 CC in the yeast cells expressing the scFv fusion proteins having either the
 CC DNA binding domain or the activation domain of the transcription
 CC activator which is not comprised in the scFv fusion proteins, and a
 CC target peptide, and selecting those yeast cells in which a reporter gene
 CC is expressed. Each scFv fusion protein comprises either an activation
 CC domain or a DNA binding domain of a transcription activator and a scFv
 CC having a heavy chain of a variable region (VH) of antibody whose sequence
 CC varies within the library, a light chain of a variable region (VL) of
 CC antibody whose sequence varies within the library independently of the VH
 CC and a linker peptide which links the VH and VL. The expression of the VH
 CC reporter gene is activated by a reconstituted transcriptional activator
 CC formed by binding of the scFv fusion protein to the target fusion
 CC protein. The methods and compositions of the present invention are useful
 CC for preventing and/or treating HIV infection and cancer. This sequence
 CC corresponds to the V1 region of an anti-human CXCR4 loop 6 antibody gene
 CC and used to generate the scFv antibody of the invention.
 XX Sequence 111 AA;
 SQ Query Match 100.0%; Score 35; DB 7; Length 111;
 Best Local Similarity 100.0%; Pred. No. 6.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DVSKRPS 7
 DB 52 DVSKRPS 58
 RESULT 14
 ADG42838
 ID ADG42838 standard; protein; 111 AA.
 XX AC ADG42838;
 XX 26-FEB-2004 (first entry)
 DT scFv Ab124 light chain variable region.
 DE HIV infection; HIV type 1; HIV type 2; cancer; breast; prostate; liver;
 KW renal; lung; skin; ovarian; cervical; brain; thyroid; stomach; colon;
 KW lymphoma; leukaemia; pancreas; chemokine receptor; antibody.
 XX Synthetic.
 XX US2003206909-A1.
 XX 06-NOV-2003.
 PD 07-FEB-2003; 2003US-00360828.
 PF 08-FEB-2002; 2002US-00071866.
 PR 08-FEB-2002; 2002US-00072301.
 PR 25-APR-2002; 2002US-00133978.
 XX (HUAS/) HUA S.
 PA (PAUL/) PAULING M H.
 PA (ZHUL/) ZHU L.
 XX Hua S, Pauling MH, Zhu L;
 PI WPI; 2004-051479/05.
 DR

CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorders, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: the sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 214 AA;

Query Match 100.0%; Score 35; DB 8; Length 214;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 71 DVSKRPS 77

Search completed: October 14, 2005, 16:12:42
Job time : 54.8125 secs

DR N-PSDB; ADG42836.
XX Antibody binding loop of human chemokine receptor useful for the
PT treatment of HIV infection and cancer.
XX
PS Claim 6; SEQ ID NO 61; 74pp; English.
XX
CC The invention relates to an antibody that binds to loop 6 of human
CC chemokine receptor (CXCR4). The antibody is useful in the treatment or
CC prevention of HIV infection (e.g. HIV type 1 and HIV type 2) and cancer
CC of (e.g. breast, prostate, liver, lung, skin, ovarian, cervical,
CC brain, thyroid, stomach, colon, lymphoma, leukaemia and pancreas cancer
CC cells), for screening drugs, for diagnosing disease or condition
CC associated with interaction with chemokine receptor. The present sequence
CC is used in the exemplification of the present invention.
XX
SQ Sequence 111 AA;

Query Match 100.0%; Score 35; DB 8; Length 111;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 52 DVSKRPS 58

RESULT 15
ABM85072
ID ABM85072 standard; protein; 214 AA.
AC ABM85072;
XX
XX 18-NOV-2004 (first entry)
XX Human diagnostic and therapeutic pprotein SEQ ID NO:5321.
XX gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX Homo sapiens.
XX WO2004023973-A2.
XX 25-MAR-2004.
XX 12-SEP-2003; 2003WO-US028227.
XX 12-SEP-2002; 2002US-0410259P.
XX 12-SEP-2002; 2002US-0410260P.
XX (INCY-) INCYTE CORP.
XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX
XX WPI; 2004-329368/30.
DR N-PSDB; ACN43724.
XX
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
XX Claim 27; Page; 190pp; English.
XX
XX The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A

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OM protein - protein search, using sw model

Run on: October 14, 2005, 16:00:04 ; Search time 13.7812 Seconds
(without alignments)
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Title: US-10-614-959-14
Perfect score: 35
Sequence: 1 DVSKRPS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pgp:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	7	4	US-09-383-667-14
2	35	100.0	111	2	US-08-652-816A-15
3	35	100.0	112	3	US-09-025-769B-19
4	35	100.0	112	4	US-09-490-070A-19
5	35	100.0	112	4	US-09-490-153-19
6	35	100.0	112	4	US-09-490-324-19
7	31	88.6	7	4	US-09-383-667-25
8	31	88.6	7	4	US-09-424-840B-125
9	31	88.6	235	2	US-08-378-939-12
10	31	88.6	236	3	US-08-487-550-10
11	31	88.6	236	4	US-08-526-098-10
12	31	88.6	236	4	US-09-383-916-10
13	31	88.6	1039	4	US-09-949-016-7859
14	31	88.6	1882	3	US-09-369-364A-13
15	30	85.7	110	3	US-09-025-769B-33
16	30	85.7	110	3	US-09-025-769B-53
17	30	85.7	110	4	US-08-490-070A-33
18	30	85.7	110	4	US-09-490-070A-53
19	30	85.7	110	4	US-09-490-153-33
20	30	85.7	110	4	US-09-490-153-53
21	30	85.7	110	4	US-09-490-324-33
22	30	85.7	110	4	US-09-490-324-53
23	29	82.9	215	3	US-09-247-373B-42
24	28	80.0	111	4	US-09-232-290-17
25	28	80.0	140	4	US-09-252-991A-23989
26	28	80.0	217	4	US-09-134-000C-5577
27	28	80.0	294	4	US-09-134-000C-4555

28	28	80.0	366	4	US-09-270-767-43922	Sequence 43922, A
29	28	80.0	514	4	US-09-252-991A-18161	Sequence 18161, A
30	28	80.0	692	4	US-09-540-236-2750	Sequence 2750, Ap
31	28	80.0	894	2	US-08-867-941-15	Sequence 15, Appl
32	28	80.0	898	2	US-08-867-941-11	Sequence 11, Appl
33	28	80.0	1118	4	US-09-538-092-423	Sequence 423, Appl
34	28	80.0	2150	4	US-09-321-987B-2	Sequence 2, Appl1
35	28	80.0	2165	4	US-09-800-729-155	Sequence 155, Appl
36	28	80.0	2432	3	US-09-074-658-15	Sequence 15, Appl
37	28	80.0	2439	3	US-09-074-658-11	Sequence 11, Appl
38	27	77.1	70	4	US-09-107-532A-7296	Sequence 7296, Ap
39	27	77.1	77	4	US-09-248-796A-17949	Sequence 17949, A
40	27	77.1	78	4	US-09-270-767-38080	Sequence 38080, A
41	27	77.1	78	4	US-09-270-767-53297	Sequence 53297, A
42	27	77.1	81	3	US-08-858-207A-476	Sequence 476, App
43	27	77.1	108	4	US-09-248-796A-22912	Sequence 22912, A
44	27	77.1	116	4	US-09-583-110-4891	Sequence 4891, Ap
45	27	77.1	124	4	US-09-107-433-3333	Sequence 3333, Ap

ALIGNMENTS

RESULT 1
US-09-383-667-14
; Sequence 14, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camelia W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Eaton, Dan L.
; APPLICANT: Hase, Philip E.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Kirchofer, Daniel
; APPLICANT: Suggett, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: P1661R2
; CURRENT APPLICATION NUMBER: US/09/383.667
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098.233
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: US 60/122.767
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 14
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-667-14
Query Match 100.0%; Score 35; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DVSKRPS 7
Db 1 DVSKRPS 7
RESULT 2
US-08-652-816A-15
; Sequence 15, Application US/08652816A
; Patent No. 5872215
; GENERAL INFORMATION:
; APPLICANT: Osbourn, JK
; APPLICANT: Allen, DJ
; APPLICANT: McCafferty, JG
; TITLE OF INVENTION: Specific binding members, materials and
; TITLE OF INVENTION: methods.
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Garstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,816A
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.4
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.8
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 23-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9525004.9
FILING DATE: 07-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610824.6
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/02240
FILING DATE: 02-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/244,597
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/33308
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-652-816A-15

Query Match 100.0%; Score 35; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 51 DVSKRPS 57

RESULT 3
US-09-025-769B-19
; Sequence 19, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Illeg, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-490-070A-19

Query Match 100.0%; Score 35; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
DB 52 DVSKRPS 58

RESULT 5
US-09-490-153-19
; Sequence 19, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; APPLICATION DATA:
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-490-070A-19

Query Match 100.0%; Score 35; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
DB 52 DVSKRPS 58

RESULT 6
US-09-490-324-19
; Sequence 19, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
; APPLICATION DATA:
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-490-324-19

Query Match 100.0%; Score 35; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
DB 52 DVSKRPS 58

RESULT 7
US-09-383-667-25
; Sequence 25, Application US/09383667

Patent No. 6624295
GENERAL INFORMATION:
APPLICANT: Lewis, Alan Peter
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
STREET: 555 THIRTEENTH ST. N.W.
CITY: WASHINGTON
STATE: D. C.
COUNTRY: U.S.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,939
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952640
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1808-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 783-6040
TELEFAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-378-939-12

Query Match 88.6%; Score 31; DB 2; Length 235;
Best Local Similarity 85.7%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 71 EVSKRPS 77

RESULT 10
US-08-487-550-10
Sequence 10, Application US/08487550
Patent No. 6113898
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
IMMUNOSUPPRESSANTS"
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
IMMUNOSUPPRESSANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435

Patent No. 6624295
GENERAL INFORMATION:
APPLICANT: Adams, Camelia W.
TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Devaux, Brigitte
STREET: 555 THIRTEENTH ST. N.W.
CITY: WASHINGTON
STATE: D. C.
COUNTRY: U.S.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,939
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952640
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1808-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 783-6040
TELEFAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-378-939-12

Query Match 88.6%; Score 31; DB 4; Length 7;
Best Local Similarity 85.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 1 EVSKRPS 7

RESULT 8
US-09-424-840B-125
Sequence 125, Application US/09424840B
Patent No. 6790938
GENERAL INFORMATION:
APPLICANT: Berchtold, Peter
TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Escher, Robert F. A.
STREET: 555 THIRTEENTH ST. N.W.
CITY: WASHINGTON
STATE: D. C.
COUNTRY: U.S.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/424,840B
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/378,939
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435

Query Match 88.6%; Score 31; DB 4; Length 7;
Best Local Similarity 85.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 1 EVSKRPS 7

RESULT 9
US-08-378-939-12
Sequence 12, Application US/08378939
Patent No. 5876961
GENERAL INFORMATION:
APPLICANT: CROWE, JAMES SCOTT

ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-487-550-10

Query Match 88.6%; Score 31; DB 3; Length 236;
Best Local Similarity 71.4%; Pred. No. 33;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 71 DINKRPS 77

RESULT 11
US-09-526-098-10
Sequence 10, Application US/09526098
Patent No. 6492134
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
IMMUNOSUPPRESSANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/526,098
FILING DATE: 07-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-526-098-10

Query Match 88.6%; Score 31; DB 4; Length 236;
Best Local Similarity 71.4%; Pred. No. 33;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 71 DINKRPS 77

RESULT 12
US-09-383-916-10
Sequence 10, Application US/09383916
Patent No. 6709654
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
IMMUNOSUPPRESSANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/383,916
FILING DATE: 26-AUG-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-383-916-10

Query Match 88.6%; Score 31; DB 4; Length 236;
Best Local Similarity 71.4%; Pred. No. 33;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 71 DINKRPS 77

RESULT 13
US-09-949-016-7859
Sequence 7859, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755

STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-33
Query Match 85.7%; Score 30; DB 3; Length 110;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 DVSKRPS 7
Db 52 DVSNRPS 58
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Job time : 14.7812 secs

PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7859
LENGTH: 1039
TYPE: PRT
ORGANISM: Human
US-09-949-016-7859
Query Match 88.6%; Score 31; DB 4; Length 1039;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DVSKRP 6
Db 915 DVSKRP 920
RESULT 14
US-09-369-364A-13
Sequence 13, Application US/09369364A
Patent No. 6391610
GENERAL INFORMATION:
APPLICANT: Apte, Suneel
APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hirohata, Satoshi
TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
FILE REFERENCE: 26473/4007/10-30-00
CURRENT APPLICATION NUMBER: US/09/369,364A
CURRENT FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 1882
TYPE: PRT
ORGANISM: Homo sapiens ADAMTS-9
FEATURE:
NAME/KEY: MOD RES
LOCATION: (468)
OTHER INFORMATION: Xaa = C
NAME/KEY: MOD RES
LOCATION: (521)
OTHER INFORMATION: Xaa = Y
US-09-369-364A-13
Query Match 88.6%; Score 31; DB 3; Length 1882;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DVSKRP 6
Db 1543 DVSKRP 1548
RESULT 15
US-09-025-769B-33
Sequence 33, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2005, 16:20:10 ; Search time 49.7656 Seconds
(without alignments)
58.615 Million cell updates/sec

Title: US-10-614-959-14
Perfect score: 35
Sequence: 1 DVSKRPS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1859788 seqs, 41671961 residues

Total number of hits satisfying chosen parameters: 1859788

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: /cgn2_6/ptodata/2/pubpaa/PTCT_NEW_PUB.pcp.*
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- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	99	15	US-10-308-817-98
2	35	100.0	99	15	US-10-453-698-98
3	35	100.0	110	15	US-10-447-331-1
4	35	100.0	111	15	US-10-360-828-61
5	35	100.0	118	18	US-10-916-758-42
6	35	100.0	240	10	US-09-880-748-1898
7	35	100.0	240	15	US-10-293-418-1898
8	35	100.0	241	10	US-09-880-748-2055
9	35	100.0	241	15	US-10-293-418-2055
10	35	100.0	242	18	US-10-981-692-24
11	35	100.0	242	18	US-10-981-692-40
					Sequence 98, Appl
					Sequence 98, Appl
					Sequence 1, Appl
					Sequence 61, Appl
					Sequence 42, Appl
					Sequence 1898, Ap
					Sequence 1898, Ap
					Sequence 2055, Ap
					Sequence 2055, Ap
					Sequence 24, Appl
					Sequence 40, Appl

12	35	100.0	243	10	US-09-880-748-1927	Sequence 1927, Ap
13	35	100.0	243	15	US-10-293-418-1927	Sequence 1927, Ap
14	35	100.0	243	18	US-10-981-692-29	Sequence 29, Appl
15	35	100.0	243	18	US-10-981-692-33	Sequence 33, Appl
16	35	100.0	244	18	US-10-981-692-26	Sequence 26, Appl
17	35	100.0	245	10	US-09-880-748-1926	Sequence 1926, Ap
18	35	100.0	245	15	US-10-293-418-1926	Sequence 1926, Ap
19	35	100.0	245	15	US-10-293-418-1926	Sequence 1926, Ap
20	35	100.0	245	18	US-10-981-692-31	Sequence 3241, Ap
21	35	100.0	245	18	US-10-981-692-36	Sequence 36, Appl
22	35	100.0	246	10	US-09-880-748-1913	Sequence 1913, Ap
23	35	100.0	246	10	US-09-880-748-1917	Sequence 1917, Ap
24	35	100.0	246	15	US-10-293-418-1913	Sequence 1913, Ap
25	35	100.0	246	15	US-10-293-418-1917	Sequence 1917, Ap
26	35	100.0	247	10	US-09-880-748-1443	Sequence 1443, Ap
27	35	100.0	247	10	US-09-880-748-1682	Sequence 1682, Ap
28	35	100.0	247	10	US-09-880-748-1685	Sequence 1685, Ap
29	35	100.0	247	10	US-09-880-748-1707	Sequence 1707, Ap
30	35	100.0	247	10	US-09-880-748-1899	Sequence 1899, Ap
31	35	100.0	247	10	US-09-880-748-1928	Sequence 1928, Ap
32	35	100.0	247	10	US-09-880-748-1934	Sequence 1934, Ap
33	35	100.0	247	15	US-10-293-418-1443	Sequence 1443, Ap
34	35	100.0	247	15	US-10-293-418-1682	Sequence 1682, Ap
35	35	100.0	247	15	US-10-293-418-1685	Sequence 1685, Ap
36	35	100.0	247	15	US-10-293-418-1707	Sequence 1707, Ap
37	35	100.0	247	15	US-10-293-418-1899	Sequence 1899, Ap
38	35	100.0	247	15	US-10-293-418-1928	Sequence 1928, Ap
39	35	100.0	247	15	US-10-293-418-1934	Sequence 1934, Ap
40	35	100.0	247	17	US-10-935-290-46	Sequence 46, Appl
41	35	100.0	247	17	US-10-935-290-77	Sequence 77, Appl
42	35	100.0	247	17	US-10-935-290-88	Sequence 88, Appl
43	35	100.0	247	17	US-10-935-290-91	Sequence 91, Appl
44	35	100.0	247	17	US-10-935-290-96	Sequence 96, Appl
45	35	100.0	247	17	US-10-935-290-105	Sequence 105, Appl

ALIGNMENTS

RESULT 1
US-10-308-817-98
; Sequence 98, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; APPLICANT: Wu, Dayang
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 98
; LENGTH: 99
; TYPE: PRT
; ORGANISM: human
US-10-308-817-98

Query Match 100.0%; Score 35; DB 15; Length 99;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 52 DVSKRPS 58
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RESULT 2
US-10-453-698-98
; Sequence 98, Application US/10453698
; Publication No. US20040038308A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell

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; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 82 CIP (1087-37 CIP)
; CURRENT APPLICATION NUMBER: US/10/453,698
; CURRENT FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 98
; LENGTH: 99
; TYPE: PRT
; ORGANISM: human
US-10-453-698-98

Query Match      100.0%; Score 35; DB 15; Length 99;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DVSKRPS 7
Db      52 DVSKRPS 58

RESULT 3
US-10-447-331-1
; Sequence 1, Application US/10447331
; Publication No. US20030219434A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Ridgway, John B.
; TITLE OF INVENTION: ANTIBODIES FOR CANCER THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS
; FILE REFERENCE: GENENT.122A
; CURRENT APPLICATION NUMBER: US/10/447,331
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: US/09/515,825
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/122262
; PRIOR FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-447-331-1

Query Match      100.0%; Score 35; DB 15; Length 110;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DVSKRPS 7
Db      52 DVSKRPS 58

RESULT 4
US-10-360-828-61
; Sequence 61, Application US/10360828
; Publication No. US20030206909A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shaobing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS
; FILE REFERENCE: 25636-727
; CURRENT APPLICATION NUMBER: US/10/360,828
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 10/071,866
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/072,301
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/133,978
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 64

; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 82 CIP (1087-37 CIP)
; CURRENT APPLICATION NUMBER: US/10/453,698
; CURRENT FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL of scFv Ab124
US-10-360-828-61

Query Match      100.0%; Score 35; DB 15; Length 111;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DVSKRPS 7
Db      52 DVSKRPS 58

RESULT 5
US-10-916-758-42
; Sequence 42, Application US/10916758
; Publication No. US20050180977A1
; GENERAL INFORMATION:
; APPLICANT: Nixon, Andrew
; APPLICANT: Madison, Edwin L.
; TITLE OF INVENTION: ENDOTHELIASE-2 LIGANDS
; FILE REFERENCE: 10280-065001
; CURRENT APPLICATION NUMBER: US/10/916,758
; CURRENT FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: US 60/520,164
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US 60/495,005
; PRIOR FILING DATE: 2003-08-14
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-916-758-42

Query Match      100.0%; Score 35; DB 18; Length 118;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DVSKRPS 7
Db      52 DVSKRPS 58

RESULT 6
US-09-880-748-1898
; Sequence 1898, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1898
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1898

Query Match
Best Local Similarity 100.0%; Score 35; DB 10; Length 240;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 181 DVSKRPS 187

RESULT 7
US-10-293-418-1898
; Sequence 1898, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1898
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1898

Query Match
Best Local Similarity 100.0%; Score 35; DB 15; Length 240;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 181 DVSKRPS 187

RESULT 8
US-09-880-748-2055
; Sequence 2055, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; CURRENT APPLICATION NUMBER: 60/276,248
; CURRENT FILING DATE: 2001-06-15
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2055
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2055

Query Match
Best Local Similarity 100.0%; Score 35; DB 15; Length 241;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 182 DVSKRPS 188

RESULT 10
US-10-981-692-24
; Sequence 24, Application US/10981692
; Publication No. US20050163777A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
; FILE REFERENCE: PF590p1
; CURRENT APPLICATION NUMBER: US/10/981,692

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; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2055
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2055

Query Match
Best Local Similarity 100.0%; Score 35; DB 10; Length 241;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 182 DVSKRPS 188

RESULT 9
US-10-293-418-2055
; Sequence 2055, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2055
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2055

Query Match
Best Local Similarity 100.0%; Score 35; DB 15; Length 241;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 182 DVSKRPS 188

RESULT 10
US-10-981-692-24
; Sequence 24, Application US/10981692
; Publication No. US20050163777A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
; FILE REFERENCE: PF590p1
; CURRENT APPLICATION NUMBER: US/10/981,692

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; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: PCT/US03/16802
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/383,802
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: N015E08 scFv
US-10-981-692-24

Query Match          100.0%; Score 35; DB 18; Length 242;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DVSKRPS 7
Db      182 DVSKRPS 188

RESULT 11
US-10-981-692-40
; Sequence 40, Application US/10981692
; Publication No. US2005016377A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
; FILE REFERENCE: PF590P1
; CURRENT APPLICATION NUMBER: US/10/981,692
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: PCT/US03/16802
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/383,802
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: N015D10 scFv
US-10-981-692-40

Query Match          100.0%; Score 35; DB 18; Length 242;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DVSKRPS 7
Db      182 DVSKRPS 188

RESULT 12
US-09-880-748-1927
; Sequence 1927, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
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; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1927
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1927

Query Match          100.0%; Score 35; DB 10; Length 243;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DVSKRPS 7
Db      183 DVSKRPS 189

RESULT 13
US-10-293-418-1927
; Sequence 1927, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1927
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1927

Query Match          100.0%; Score 35; DB 15; Length 243;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DVSKRPS 7
Db      183 DVSKRPS 189

RESULT 14
US-10-981-692-29
; Sequence 29, Application US/10981692
; Publication No. US2005016377A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
; FILE REFERENCE: PF590P1
; CURRENT APPLICATION NUMBER: US/10/981,692
; CURRENT FILING DATE: 2004-11-05
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✓ ; PRIOR APPLICATION NUMBER: PCT/US03/16802
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/383,802
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: N024E07 scFv
US-10-981-692-29

Query Match 100.0%; Score 35; DB 18; Length 243;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 183 DVSKRPS 189

RESULT 15
US-10-981-692-33
; Sequence 33, Application US/10981692
; Publication No. US20050163777A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
; FILE REFERENCE: PFS90Pl
; CURRENT APPLICATION NUMBER: US/10/981,692
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: PCT/US03/16802
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/383,802
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: N023E01 scFv
US-10-981-692-33

Query Match 100.0%; Score 35; DB 18; Length 243;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 183 DVSKRPS 189

Search completed: October 14, 2005, 17:00:44
Job time : 50.7656 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2005, 16:02:59 ; Search time 9.73438 Seconds
(without alignments)
69.190 Million cell updates/sec

Title: US-10-614-959-14

Perfect score: 35
Sequence: 1 DVSKRPS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: piri:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	99	2 S36057	Ig lambda chain -
2	34	97.1	646	2 G85056	probable receptor-
3	32	91.4	60	2 A24626	Ig lambda chain V-
4	32	91.4	103	2 A38923	AL type amyloid fi
5	32	91.4	111	1 L2HUTR	Ig lambda chain V-
6	32	91.4	423	2 F64690	type IIS restricti
7	31	88.6	110	2 S51149	antibody light cha
8	31	88.6	111	1 L2HUVN	Ig lambda chain V-
9	31	88.6	111	2 S36281	Ig lambda chain V-
10	30	85.7	112	2 S31515	Ig lambda chain V-
11	30	85.7	112	2 S44105	Ig lambda chain V-
12	30	85.7	416	2 S26836	Ig lambda chain V-
13	29	82.9	74	2 AH2642	type II site-speci
14	29	82.9	88	2 A97425	hypothetical prote
15	29	82.9	337	1 E70191	conserved hypotet
16	29	82.9	377	2 A32548	homeobox protein M
17	29	82.9	404	2 T00750	probable protein p
18	29	82.9	685	2 T21466	hypothetical prote
19	29	82.9	690	2 T21806	hypothetical prote
20	29	82.9	735	2 T00850	probable receptor-
21	29	82.9	972	2 H84903	hypothetical prote
22	29	82.9	1033	2 T37715	actin-interacting
23	29	82.9	1077	2 T21800	hypothetical prote
24	29	82.9	1245	2 G84897	hypothetical prote
25	28	80.0	91	2 T09711	ADP,ATP carrier pr
26	28	80.0	111	1 L2HUMC	Ig lambda chain V-
27	28	80.0	189	2 AE1316	GTP cyclohydrolase
28	28	80.0	189	2 AE1688	GTP cyclohydrolase
29	28	80.0	235	2 S25759	Ig lambda chain -

30	28	80.0	235	2 S14675	Ig lambda chain -
31	28	80.0	259	2 T40075	60s ribosomal prot
32	28	80.0	292	2 A64624	hypothetical prote
33	28	80.0	296	2 D71891	hypothetical prote
34	28	80.0	300	2 A82017	probable lipoprote
35	28	80.0	301	2 AE0243	hypothetical prote
36	28	80.0	309	2 E83999	mutants block spor
37	28	80.0	310	2 B97777	thioredoxin-dialuf
38	28	80.0	310	2 D71703	thioredoxin reduct
39	28	80.0	348	2 G87604	thioredoxin reduct
40	28	80.0	440	2 S65358	familial Alzheimer
41	28	80.0	447	2 S35481	SRP54 protein - M
42	28	80.0	452	2 T40769	hypothetical prote
43	28	80.0	458	1 Z28PC2	gene 12 protein -
44	28	80.0	463	2 F90422	4-hydroxybutyryl-C
45	28	80.0	498	1 HYBSPA	pseudolysin (EC 3.

ALIGNMENTS

RESULT 1

S36057
Ig lambda chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C:Accession: S36057
R:Williams, S.C.
Submitted to the EMBL Data Library, April 1993
A:Reference number: S36046
A:Accession: S36057
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-99 <WIL>
A:Cross-references: EMBL:Z22198; NID:G312319; PIDN:CAA80208.1; PID:G312320
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-92/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 35; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	DVSKRPS	7
Db	52	DVSKRPS	58

RESULT 2

G85056
Probable receptor-like protein kinase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Aug-2004
C:Accession: G85056
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A>Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: G85056
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-646 <STO>
A:Cross-references: UNIPROT:Q9XEC7; GB:NC_001268; NID:G7267207; PIDN:CAB77918.1; GSPDB:G

Query Match 97.1%; Score 34; DB 2; Length 646;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1	DVSKRPS	7
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A;Gene: GDB:IGLV@
A;Cross-references: GDB:119342; OMIM:147240
A;Map position: 22q11.2-22q11.2
C;Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kappa)
chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into lai
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: blocked amino end; heterotrimer; immunoglobulin
F;15-92/Domain: immunoglobulin homology <IMM>
F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status
F;22-90/Disulfide bonds: #status predicted

Query Match 91.4%; Score 32; DB 1; Length 111;
Best Local Similarity 85.7%; Pred. No. 5.9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
DB 52 DVTKRPS 58

RESULT 6
F64690
type IIS restriction enzyme R protein - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: F64690
R;Tomb: J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne;
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.N
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: F64690
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-423 <TOM>
A;Cross-references: UNIPROT:O25919; GB:AE000637; GB:AE000511; NID:92314536; PIDN:AAD0841C

Query Match 91.4%; Score 32; DB 2; Length 423;
Best Local Similarity 85.7%; Pred. No. 23;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
DB 71 DMSKRPS 77

RESULT 7
S51149
antibody light chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C;Accession: S51149
R;de Kruij, J.; Boel, E.; Logtenberg, T.
submitted to the EMBL Data Library, January 1995
A;Description: Selection and application of human SCFV antibody fragments from a semi-sy
A;Reference number: S51147
A;Accession: S51149
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-110 <DEK>
A;Cross-references: EMBL:X83712
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;13-90/Domain: immunoglobulin homology <IMM>

Query Match 88.6%; Score 31; DB 2; Length 110;
Best Local Similarity 85.7%; Pred. No. 9.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
DB 50 EVSKRPS 56

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DB 606 DISKRPS 112

RESULT 3
A24626
Ig lambda chain V-II region (Har) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 16-Aug-1996
C;Accession: A24626
R;Eulitz, M.; Linke, R.
Biochem. Biophys. Res. Commun. 194, 1427-1434, 1993
A;Title: The precursor molecule of a V-lambda II-immunoglobulin light chain-derived amy
A;Reference number: A24626; MUID:86077295; PMID:8355132
A;Accession: A24626
A;Molecule type: protein
A;Residues: 1-60 <EUL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin

Query Match 91.4%; Score 32; DB 2; Length 60;
Best Local Similarity 85.7%; Pred. No. 3.1;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
DB 45 DVNKRPS 51

RESULT 4
A38923
AL type amyloid fibril protein precursor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000
C;Accession: A38923
R;Eulitz, M.; Linke, R.P.
Biochem. Biophys. Res. Commun. 194, 1427-1434, 1993
A;Title: The precursor molecule of a V-lambda II-immunoglobulin light chain-derived amy
A;Reference number: A38923; MUID:93356823; PMID:8352801
A;Accession: A38923
A;Molecule type: protein
A;Residues: 1-95;96-103 <EUL>
C;Comment: This protein is derived from an immunoglobulin light chain of lambda type.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: amyloid; immunoglobulin
F;1-58/Product: AL type amyloid fibril protein #status predicted <MAT>
F;7-83/Domain: immunoglobulin homology <IMM>

Query Match 91.4%; Score 32; DB 2; Length 103;
Best Local Similarity 85.7%; Pred. No. 5.4;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
DB 43 DVNKRPS 49

RESULT 5
L2HUTR
Ig lambda chain V-II region (Tro) - human (tentative sequence)
C;Species: Homo sapiens (man)
C;Date: 29-Jul-1981 #sequence_revision 29-Jul-1981 #text_change 09-Jul-2004
C;Accession: A01973
R;Scholz, R.; Yang, C.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 360, 1903-1918, 1979
A;Title: Zur Strukturregel der Antikörper. Die Primärstruktur eines monoklonalen Iga
A;Reference number: A01973; MUID:80114123; PMID:118915
A;Accession: A01973
A;Molecule type: protein
A;Residues: 1-111 <SCH>
A;Cross-references: UNIPROT:P01707
C;Comment: This chain was isolated from a myeloma protein.
C;Genetics:

```

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submitted to the EMBL Data Library, January 1993
A:Description: V-lambda-2 gene sequence of a high affinity anti-idiotypic IgM antibody f
A:Reference number: S31515
A:Accession: S31515
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-112 <VAN>
A:Cross-references: EMBL:Z19546; NID:G33754; PIDN:CAA79606.1; PID:G33755
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-92/Domain: immunoglobulin homology <IMM>

Query Match      85.7%; Score 30; DB 2; Length 112;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
DB 52 DVSNRPS 58

RESULT 11
S44105
Ig lambda chain V-J region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C:Accession: S44105
R:Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
Submitted to the EMBL Data Library, March 1994
A:Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable re
A:Reference number: S44105
A:Accession: S44105
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-112 <HAW>
A:Cross-references: EMBL:Z31388; NID:G472959; PIDN:CAA93263.1; PID:G940517
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-92/Domain: immunoglobulin homology <IMM>

Query Match      85.7%; Score 30; DB 2; Length 112;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
DB 52 DVSNRPS 58

RESULT 12
S26836
type II site-specific deoxyribonuclease (EC 3.1.21.4) MboII - Moraxella bovis
C:Species: Moraxella bovis
C:Date: 03-Mar-1994 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S26836
R:Bocklage, H.; Heeger, K.; Mueller-Hill, B.
Nucleic Acids Res. 19, 1007-1013, 1991
A:Title: Cloning and characterization of the MboII restriction-modification system.
A:Reference number: S26835; MUID:91212177; PMID:2020540
A:Accession: S26836
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-416 <BOC>
A:Cross-references: UNIPROT:P23191; EMBL:X56977; NID:G44180; PIDN:CAA40298.1; PID:G44182
C:Keywords: hydrolase

Query Match      85.7%; Score 30; DB 2; Length 416;
Best Local Similarity 83.3%; Pred. No. 64;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 6
DB 66 DISKRP 71

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RESULT 8
L2HUNW
Ig lambda chain V-II region (Win) - human (tentative sequence)
C:Species: Homo sapiens (man)
C:Date: 30-Nov-1979 #sequence_revision 30-Nov-1979 #text_change 09-Jul-2004
C:Accession: A01978
R:Chen, B.L.; Chiu, Y.Y.H.; Humphrey, R.L.; Poljak, R.J.
Biochim. Biophys. Acta 537, 9-21, 1978
A:Title: Amino acid sequence of the human myeloma lambda chain Win.
A:Reference number: A01978; MUID:79062503; PMID:102365
A:Accession: A01978
A:Molecule type: protein
A:Residues: 1-111 <CHE>
A:Cross-references: UNIPROT:P01712
C:Comment: This is a Bence Jones protein.
C:Genetics:
A:Gene: GDB:IGLV6
A:Cross-references: GDB:119342; OMIM:147240
A:Map position: 22q11.2-22q11.2
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: blocked amino end; heterotetramer
F:15-92/Domain: immunoglobulin homology <IMM>
F:1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #statu
F:22-90/Disulfide bonds: #status predicted

Query Match      88.6%; Score 31; DB 1; Length 111;
Best Local Similarity 85.7%; Pred. No. 9.9;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
DB 52 DVDRKPS 58

RESULT 9
S36281
Ig lambda chain V region (clone alpha-FOG1-A3) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C:Accession: S36281
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; MUID:93178448; PMID:7679990
A:Accession: S36281
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-111 <GRI>
A:Cross-references: EMBL:Z19823; NID:G33414; PIDN:CAA79275.1; PID:G939907
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-92/Domain: immunoglobulin homology <IMM>

Query Match      88.6%; Score 31; DB 2; Length 111;
Best Local Similarity 85.7%; Pred. No. 9.9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
DB 52 EVSKRPS 58

RESULT 10
S31515
Ig lambda chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C:Accession: S31515
R:van der Heijden, R.W.J.; Uytendaele, F.G.C.M.; Osterhaus, A.D.M.E.

```

Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochaete, *Borrelia burgdorferi*.
A:Reference number: A70100; MUID:98065943; PMID:9403685
A:Accession: E70191
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-337 <KLE>
A:Cross-references: UNIPROT:O51676; GB:AE001173; GB:AE000783; NID:g2688665; PIDN:AAC67081
A:Experimental source: strain B31
C:Superfamily: translation factor, SUA5 type

Query Match 82.9%; Score 29; DB 1; Length 337;
Best Local Similarity 71.4%; Pred. No. 88;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKEPS 7
Db 141 NISKEPS 147

Search completed: October 14, 2005, 16:23:40
Job time : 11.7344 sec

hypothetical protein Atu0540 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
A:Title: Agrobacterium tumefaciens
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AH2642
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AH2642
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-74 <KUR>
A:Cross-references: UNIPROT:Q8UHW8; GB:AE008688; PIDN:AAL41558.1; PID:gl7738891; GSPDB:C
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu0540
A:Map position: circular chromosome

Query Match 82.9%; Score 29; DB 2; Length 74;
Best Local Similarity 71.4%; Pred. No. 19;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKEPS 7
Db 2 DISKEPS 8

hypothetical protein AGR_C_956 [imported] - Agrobacterium tumefaciens (strain C58, Cerec
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C:Accession: A97425
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: A97425
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-88 <KUR>
A:Cross-references: UNIPROT:Q8UHW8; GB:AE007869; PIDN:AAK86354.1; PID:gl5155478; GSPDB:C
C:Genetics:
A:Gene: AGR_C_956
A:Map position: circular chromosome

Query Match 82.9%; Score 29; DB 2; Length 88;
Best Local Similarity 71.4%; Pred. No. 23;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKEPS 7
Db 16 DISKEPS 22

hypothetical protein BB0734 - Lyme disease spirochete
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: E70191
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.

Query Match 82.9%; Score 29; DB 2; Length 88;
Best Local Similarity 71.4%; Pred. No. 23;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKEPS 7
Db 16 DISKEPS 22

hypothetical protein BB0734 - Lyme disease spirochete
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: E70191
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.

Query Match 82.9%; Score 29; DB 2; Length 88;
Best Local Similarity 71.4%; Pred. No. 23;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKEPS 7
Db 16 DISKEPS 22

hypothetical protein BB0734 - Lyme disease spirochete
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: E70191
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.

Query Match 82.9%; Score 29; DB 2; Length 88;
Best Local Similarity 71.4%; Pred. No. 23;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKEPS 7
Db 16 DISKEPS 22

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2005, 15:51:44 ; Search time 46.5938 Seconds
(without alignments)
76.932 Million cell updates/sec

Title: US-10-614-959-14
Perfect score: 35
Sequence: 1 DVSKRPS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	34	97.1	646	2	Q9XEC7	Q9Xec7 arabidopsis
2	32	91.4	111	1	LV2D HUMAN	P01707 homo sapien
3	32	91.4	236	2	Q6PIQ7	Q6piq7 homo sapien
4	32	91.4	423	2	Q25919	Q25919 helicobacte
5	31	88.6	111	1	LV2I HUMAN	P01712 homo sapien
6	31	88.6	130	2	Q7MUS6	Q7mus6 porphyromon
7	31	88.6	233	2	Q7S4H3	Q7s4h3 neurospora
8	31	88.6	400	2	Q7SZL9	Q7szl9 brachydanio
9	31	88.6	402	2	Q64WE5	Q64we5 bacteroides
10	31	88.6	486	2	Q928G3	Q928g3 streptomyce
11	31	88.6	728	2	Q7SFP0	Q7sf90 neurospora
12	31	88.6	1292	2	Q6SLD6	Q6sld6 cochliobolu
13	31	88.6	1766	2	Q7SE06	Q7se06 ashbya goss
14	31	88.6	1935	1	ATS9 HUMAN	Q9p2n4 homo sapien
15	30	85.7	164	1	BFR1 MAGNG	Q50171 magnecospir
16	30	85.7	212	2	Q3V6F8	Q3v6f8 drosophila
17	30	85.7	233	2	Q6FJA3	Q6fja3 homo sapien
18	30	85.7	236	2	Q6P5S3	Q6p5s3 homo sapien
19	30	85.7	267	2	Q9BTM2	Q9btm2 homo sapien
20	30	85.7	279	1	Y170 BUCBP	Q89as2 buchnera ap
21	30	85.7	283	2	Q70914	Q70914 prunus necr
22	30	85.7	283	2	Q70918	Q70918 prunus necr
23	30	85.7	285	2	Q71142	Q71142 prunus necr
24	30	85.7	327	2	Q86V04	Q86v04 homo sapien
25	30	85.7	378	2	Q9XY82	Q9xy82 enchytraeus
26	30	85.7	385	2	Q7S0S8	Q7s0s8 neurospora
27	30	85.7	401	2	Q6DHX1	Q6dhl1 homo sapien
28	30	85.7	416	1	T2M2 MORBO	P23191 moraxella b
29	30	85.7	508	2	Q60U48	Q60u48 mus musculu
30	30	85.7	530	2	Q6PHC0	Q6phc0 mus musculu
31	30	85.7	654	2	Q8CAA2	Q8caa2 mus musculu

32	30	85.7	674	2	Q9DBJ2	Q9dbj2 mus musculu
33	30	85.7	706	1	TM24 HUMAN	O14523 homo sapien
34	30	85.7	706	1	TM24 MOUSE	Q80x80 mus musculu
35	30	85.7	747	2	Q6D0L7	Q6d0l7 erwinia car
36	30	85.7	833	2	Q6ADP4	Q6adp4 leifsonia x
37	30	85.7	1036	2	Q6LWQ4	Q6lwq4 methanococc
38	30	85.7	1059	2	Q6LWQ4	Q6lwq4 bacteroides
39	30	85.7	1372	2	Q8SX99	Q8sx99 drosophila
40	30	85.7	1372	2	Q9VN46	Q9vn46 drosophila
41	29	82.9	59	2	Q6VEY3	Q6vey3 vitis vinif
42	29	82.9	74	2	Q8UHW8	Q8uhw8 agrobacteri
43	29	82.9	80	2	Q6LK05	Q6lk05 photobacter
44	29	82.9	88	2	Q7D190	Q7d190 agrobacteri
45	29	82.9	103	2	Q6D0T2	Q6d0t2 erwinia car

ALIGNMENTS

RESULT 1

Q9XEC7 PRELIMINARY; PRT; 646 AA.
AC Q9XEC7;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Putative receptor-like protein kinase.
GN Name=T2eN6.11; Synonyms=AT4g04500;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; rosids;
OC eurside II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhong J., Ma P., Parnell L.D., Chen C.-N., Chen E.Y.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Parnell L.D.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Zhong J., Ma P., Parnell L.D., Chen C.N., Chen E.Y., Mewes H.W.,
RA Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AF076243; AAD29762.1; -.
DR EMBL; AL161500; CAB77918.1; -.
DR PIR; G85056; G85056.
DR HSSP; P06239; 3LCK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; P:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR002902; DUF26.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_Thr_pkin_AS.
DR Pfam; PF01657; DUF26; 2.
DR Pfam; PF00069; Kinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PSS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
KW Transferase.
SQ SEQUENCE 646 AA; 73439 MW; E1200574D5864207 CRC64;

RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC030383; AAH30983.1; -
DR HSP; P01709; IABJ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS0290; IG_MHC.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 4A07BEF60A5FD465 CRC64;
Query Match 91.4%; Score 32; DB 2; Length 111;
Best Local Similarity 85.7%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DVSKRPS 7
Db 71 DVTKRPS 77
RESULT 4
O25919 ID O25919 PRELIMINARY; PRT; 423 AA.
AC O25919;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Type IIS restriction enzyme R protein (NEOIR).
GN OrderedLocustNames=HPI366;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=26695 / ATCC 700392;
RC MEDLINE=97394467; PubMed=9252185; DOI=10.1038/41483;
RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R.,
RA Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F.,
RA Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G.,

Query Match 97.1%; Score 34; DB 2; Length 646;
Best Local Similarity 85.7%; Pred. No. 69;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DVSKRPS 7
Db 606 DISKRPS 612
RESULT 2
LV2D_HUMAN STANDARD; PRT; 111 AA.
AC P01707;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda chain V-II region TRO.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RX MEDLINE=80114123; PubMed=118915;
RA Scholz R., Yang C., Hilschmann N.;
RT "Rule of antibody structure. Primary structure of a human monoclonal
RT IgA1-immunoglobulin (myeloma protein Tro). VI. Amino acid sequence of
RT the L-chain, lambda-type, subgroup II.";
RL Hoppe-Seyler's Z. Physiol. Chem. 360:1903-1918(1979).
CC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01973; L2HUTR.
DR HSP; P01709; 2MCG.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region;
KW Pyrolydione carboxylic acid.
FT DOMAIN 1 106 Ig-like.
FT MOD RES 1 1 Pyrolydione carboxylic acid.
FT DISULFID 22 90 By similarity.
FT NON TER 111 111
SQ SEQUENCE 111 AA; 99DC457A12E8F6E1 CRC64;
Query Match 91.4%; Score 32; DB 1; Length 111;
Best Local Similarity 85.7%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DVSKRPS 7
Db 52 DVTKRPS 58
RESULT 3
Q6PIQ7 ID Q6PIQ7 PRELIMINARY; PRT; 236 AA.
AC Q6PIQ7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RA Glodok A., McKenney K., FitzGerald L.M., Lee N., Adams M.D.,
RA Hickey E.K., Berg D.E., Cocayne J.D., Utterback T.R., Peterson J.D.,
RA Wattey J.M., Cotton M.D., Weidman J.F., Fujii C., Bowman C.,
RA Smith L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D.,
RA Smith H.O., Fraser C.M., Venter J.C.,
RT "The complete genome sequence of the gastric pathogen *Helicobacter pylori*."
RL Nature 388:539-547(1997).
DR EMBL: AE000637; AAD08410.1; -.
DR TIGR: HP1366; -.
DR InterPro: IPR003615; HNH_nuc.
DR SMART: SM00507; HNHc; 1.
KW Complete proteome.
SQ SEQUENCE 423 AA; 50047 MW; 9086E51C8FE4E58E CRC64;
Query Match 91.4%; Score 32; DB 2; Length 423;
Best Local Similarity 85.7%; Pred. No. 1.3e-02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 DVSKRPS 7
Db 71 DMSKPS 77
RESULT 5
LV21 HUMAN STANDARD; PRT; 111 AA.
AC P01712;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda chain V-II region WIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=79062503; PubMed=102365; DOI=10.1016/0005-2795(78)90598-6;
RA Chen B.L., Chiu Y.-Y.H., Humphrey R.L., Poljak R.J.;
RT "Amino acid sequence of the human myeloma lambda chain Win.";
RL Biochim. Biophys. Acta 537:9-21(1978).
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A01978; L2HWN.
DR HSSP: P01709; 1DCL.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; ig; 1.
DR SMART: SM00406; IGv; 1.
DR PROSITE: PS00835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region; Pyroglutamate carboxylic acid.
FT DOMAIN 1 106
FT MOD RES 1 1
FT DISULFID 22 90
FT NON_TER 111 111
FT By similarity.
SQ SEQUENCE 111 AA; 11694 MW; 8C3CE95FE721B87C CRC64;
Query Match 88.6%; Score 31; DB 1; Length 111;
Best Local Similarity 85.7%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 DVSKRPS 7
Db 52 DVDKRPS 58
RESULT 6
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

Q7MUS6
ID Q7MUS6 PRELIMINARY; PRT; 130 AA.
AC Q7MUS6;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Hypothetical protein.
DE OrderedLocNames=PGI409;
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OX NCBI_TaxID=837;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=W83;
RX MEDLINE=22829867; PubMed=12949112;
RX DOI=10.1128/JB.185.18.5591-5601.2003;
RA Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,
RA Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,
RA Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Taiton L., Gray J.,
RA Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,
RA Dewhirst F.E., Fraser C.M.;
RT "Complete genome sequence of the oral pathogenic bacterium Porphyromonas gingivalis strain W83.";
RL J. Bacteriol. 185:5591-5601(2003).
DR EMBL: AE017176; AAQ66466.1; -.
DR TIGR: PGI409; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 130 AA; 14455 MW; 3F2E1F64F23E5805 CRC64;
Query Match 88.6%; Score 31; DB 2; Length 130;
Best Local Similarity 71.4%; Pred. No. 63;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 DVSKRPS 7
Db 107 DISRPS 113
RESULT 7
Q7S4H3
ID Q7S4H3 PRELIMINARY; PRT; 233 AA.
AC Q7S4H3;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=NCU02220.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamysellis M., Mauceli E., Bielek C., Rudd S., Frishman D.,
RA Kryzstofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Planann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus *Neurospora crassa*.";
RL Nature 0:0-0(2003).
CC -1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

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CC      preliminary data.
DR      EMBL; AABX01000366; EAA30397.1; -.
DR      GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact...; IEA.
DR      GO; GO:0015035; F:protein disulfide oxidoreductase activity; IEA.
DR      InterPro; IPR001853; DSBA.
DR      InterPro; IPR010986; DeBA_insertion.
DR      Pfam; PF01323; DSBA; 1.
KW      Hypothetical protein.
SQ      SEQUENCE 233 AA; 25367 MW; 50B8F4A369168929 CRC64;

Query Match      88.6%; Score 31; DB 2; Length 233;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 DVSKRPS 7
DB      222 DVSERPS 228
      |||||
      |||||

RESULT 8
ID      Q7SZL9      PRELIMINARY;      PRT;      400 AA.
AC      Q7SZL9;
DT      01-OCT-2003 (TrEMBLrel. 25, Created)
DT      01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      ATP-gated ionotropic P2X receptor subunit 2.
GN      Name=p2rx2; Synonyms=p2xr2;
OS      Brachydanio rerio (Zebrafish) (Danio rerio).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC      Cyprinidae; Danio.
OX      NCBI_TaxID=7955;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=22943235; PubMed=14580944; DOI=10.1016/S0306-4522(03)00566-9;
RA      Kucenas S., Li Z., Cox J.A., Egan T.M., Voigt M.M.;
RT      "Molecular characterization of the zebrafish P2X receptor subunit gene
      family.";
RL      Neuroscience 121:935-945(2003).
DR      EMBL; AY292650; AAQ21195.1; -.
DR      ZFIN; ZDB-GENE-030319-2; p2rx2.
DR      GO; GO:0009503; C:light-harvesting complex (sensu Viridiplantae); IEA.
DR      GO; GO:0016020; C:membrane; IEA.
DR      GO; GO:0005524; F:ATP binding; IEA.
DR      GO; GO:0005216; F:ion channel activity; IEA.
DR      GO; GO:0016978; F:lipote-protein ligase B activity; IEA.
DR      GO; GO:0004872; F:receptor activity; IEA.
DR      GO; GO:0006091; P:energy pathways; IEA.
DR      GO; GO:0006811; P:ion transport; IEA.
DR      InterPro; IPR000066; Antenna_a/b.
DR      InterPro; IPR001429; P2X_receptor.
DR      Pfam; PF00864; P2X_receptor; 1.
DR      TIGRfam; TIGR00863; P2X; 1.
KW      Receptor.
SQ      SEQUENCE 400 AA; 45752 MW; EE571C00171609F5 CRC64;

Query Match      88.6%; Score 31; DB 2; Length 400;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 DVSKRPS 7
DB      369 DVSKQPS 375
      |||||
      |||||

RESULT 9
Q64WES      PRELIMINARY;      PRT;      402 AA.
ID      Q64WES;
AC      Q64WES;
DT      25-OCT-2004 (TrEMBLrel. 28, Created)
DT      25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT      25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE      Predicted nucleoside-diphosphate sugar epimerase.
GN      ORFNames=BF1430;
OS      Bacteroides fragilis.
OC      Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC      Bacteroidaceae; Bacteroides.
OX      NCBI_TaxID=817;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=YCH46;
RA      Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
      Kuhara S., Hattori M., Hayashi T., Ohnishi Y.;
RT      "Genomic analysis of Bacteroides fragilis reveals extensive DNA
      RT      inversions regulating cell surface adaptation.";
RL      Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2004).
DR      EMBL; AP06841; BAD48181.1; -.
SQ      SEQUENCE 402 AA; 45596 MW; 2D56A6DAF87797CC CRC64;

Query Match      88.6%; Score 31; DB 2; Length 402;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DVSKRP 6
DB      348 DVSKRP 353
      |||||
      |||||

RESULT 10
Q828G3      PRELIMINARY;      PRT;      486 AA.
ID      Q828G3;
AC      Q828G3;
DT      01-JUN-2003 (TrEMBLrel. 24, Created)
DT      01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      Putative cytochrome P450.
GN      Name=cyp24; OrderedLocusNames=SAV6706;
OS      Streptomyces avermitilis.
OC      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC      Streptomycineae; Streptomycetaceae; Streptomyces.
OX      NCBI_TaxID=33903;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      STRAIN=MA-4680;
RC      MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
RA      Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
      Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
      Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT      "Genome sequence of an industrial microorganism Streptomyces
      RT      avermitilis: deducing the ability of producing secondary
      RT      metabolites.";
RL      Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
DR      EMBL; AP005047; BAC74417.1; -.
RN      [2]
RP      SEQUENCE FROM N.A.
RX      STRAIN=MA-4680;
RC      MEDLINE=22608306; PubMed=12692562;
RA      Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
      Sakaki Y., Hattori M., Omura S.;
RT      "Complete genome sequence and comparative analysis of the industrial
      RT      microorganism Streptomyces avermitilis.";
RL      Nat. Biotechnol. 21:526-531(2003).
CC      -i- SIMILARITY: Belongs to the cytochrome P450 family.
DR      EMBL; AP005047; BAC74417.1; -.
DR      HSSP; Q9L142; 1GWI.
DR      GO; GO:0004497; F:monooxygenase activity; IEA.
DR      GO; GO:0006118; P:electron transport; IEA.
DR      InterPro; IPR002397; BP450.
DR      InterPro; IPR001128; Cytochrome_P450.
DR      PRINTS; PR00359; BP450.
DR      PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
KW      Complete proteome; Heme; Monooxygenase; Oxidoreductase.
SQ      SEQUENCE 486 AA; 53354 MW; A728B74F6592E265 CRC64;

Query Match      88.6%; Score 31; DB 2; Length 486;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
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Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 428 DVSKRPS 434

RESULT 11
Q7SF90
ID Q7SF90 PRELIMINARY; PRT; 728 AA.
AC Q7SF90;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Predicted protein.
GN Name=NCU00559.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Seltrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamysseilis M., Maucelli E., Bielke C., Rudd S., Frishman D.,
RA Kryatofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmari S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Vanden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbel D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.,
RA "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC Preliminary data.
DR EMBL; AABX01000022; EAA35484.1; -;
SQ SEQUENCE 728 AA; 79550 MW; 05A688EBD3850B79 CRC64;

Query Match 88.6%; Score 31; DB 2; Length 728;
Best Local Similarity 85.7%; Pred. No. 3.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 336 DASKRPS 342

RESULT 12
Q6SLD6
ID Q6SLD6 PRELIMINARY; PRT; 1292 AA.
AC Q6SLD6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative histidine kinase HKK1p.
GN Name=HKK1;
OS Cochliobolus heterostrophus (Drechslera maydis).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Pleosporaceae; Cochliobolus.
OX NCBI_TaxID=5016;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C4;
RA PubMed=14665450; DOI=10.1128/EC.2.6.1151-1161.2003;
RA Catiect N.L., Yoder O.C., Turgeon B.G.;
RT "Whole-genome analysis of two-component signal transduction genes in

RT fungal pathogens";
RL Eukaryotic Cell 2:1151-1161(2003).
CC -!- SIMILARITY: Contains 1 histidine kinase domain.
DR EMBL; AY456014; AAR29890.1; -;
DR GO; GO:0016014; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0000156; F:two-component response regulator activity; IEA.
DR GO; GO:0000155; F:two-component sensor molecule activity; IEA.
DR GO; GO:0007600; P:sensory perception; IEA.
DR GO; GO:0000160; P:two-component signal transduction system (p...); IEA.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR004358; Bact_sens_PRC.
DR InterPro; IPR011006; Chey_like.
DR InterPro; IPR005467; His_kinase.
DR InterPro; IPR003661; His_kinase.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF00512; Hsika; 1.
DR Pfam; PF00072; Response_reg; 1.
DR PRINTS; PR00344; BCTRLSENSOR.
DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00388; Hsika; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS50109; HIS_KIN; 1.
DR PROSITE; PS50110; RESPONSE_REGULATORY; 1.
DR KINase; Phosphorylation; Sensory transduction.
SQ SEQUENCE 1292 AA; 144730 MW; 57010F00609FF49B CRC64;

Query Match 88.6%; Score 31; DB 2; Length 1292;
Best Local Similarity 85.7%; Pred. No. 6.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 45 DVDKRP 51

RESULT 13
Q7SE06
ID Q7SE06 PRELIMINARY; PRT; 1766 AA.
AC Q7SE06;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE ABL133Cp.
GN ORFNames=ABL133C;
OS Ashbya gossypii (Yeast) (Eremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
OX NCBI_TaxID=33169;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 10895;
RA Voegeli S.E., Dietrich F.S., Brachat S., Lerch A., Gaffney T.,
RA Philippsen P.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE016815; AAS50638.1; -;
DR ACD; ABL133C; -;
SQ SEQUENCE 1766 AA; 179132 MW; BEC73A1CF69F2EA3 CRC64;

Query Match 88.6%; Score 31; DB 2; Length 1766;
Best Local Similarity 85.7%; Pred. No. 9.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 1445 DVSKRPS 1451

RESULT 14

FT CARBOHYD 1806 1806 N-linked (GlcNAc...) (Potential).
 FT VARSPPLIC 1064 1072 CLVTCKGH -> VRMEGCVFP (in isoform 3).
 FT VARSPPLIC 1073 1935 Missing (in isoform 3).
 FT VARSPPLIC 1624 1629 CSVTG -> VPSWEL (in isoform 2).
 FT VARSPPLIC 1630 1935 Missing (in isoform 2).
 FT CONFLICT 46 46 S -> G (in Ref. 1).
 FT CONFLICT 96 96 P -> S (in Ref. 1).
 FT CONFLICT 182 182 D -> G (in Ref. 2).
 FT CONFLICT 367 367 F -> L (in Ref. 1).
 FT CONFLICT 1117 1117 V -> G (in Ref. 3).
 SQ SEQUENCE 1935 AA; 216556 MW; FD3D51E88300A3C6 CRC64;
 Query Match 88.6%; Score 31; DB 1; Length 1935;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DVSKRP 6
 Db 1596 DVSKRP 1601
 RESULT 15
 BFR1_MAGMG
 ID BFR1_MAGMG STANDARD; PRT; 164 AA.
 AC OS0171;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Bacterioferritin subunit 1 (BFR 1).
 GN Name=bfr1;
 OS Magnetospirillum magnetotacticum (Aquaspirillum magnetotacticum).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
 OC Rhodospirillaceae; Magnetospirillum.
 OX NCBI_TaxID=188;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MS-1;
 RX MEDLINE=98072426; PubMed=9409768; DOI=10.1016/S0378-1119(97)00424-1;
 RA Bertani L.E., Huang J.S., Weir B.A., Kirschvink J.L.;
 RT Evidence for two types of subunits in the bacterioferritin of
 Magnetospirillum magnetotacticum.;
 RL Gene 201:31-36(1997).
 CC -1- FUNCTION: May perform analogous functions in iron detoxification
 and storage to that of animal ferritins (By similarity).
 CC -1- COPACTOR: Binds 1 heme b (iron-protoporphyrin IX) group per
 monomer (Potential).
 CC -1- SUBUNIT: Oligomer of 24 identical subunits (By similarity).
 CC -1- MISCELLANEOUS: The di-iron binding site functions as active site
 where iron ions are oxidized from iron(II) to iron(III) before
 they are stored (By similarity).
 CC -1- SIMILARITY: Belongs to the bacterioferritin family.
 CC -1- SIMILARITY: Contains 1 ferritin-like diiron domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF001959; AAC91253.1; -;
 CC HSP; F11056; IBCF.
 DR InterPro; IPR002024; Bacterioferritin.
 DR InterPro; IPR009078; Ferritin/RR like.
 DR InterPro; IPR008331; Ferritin Dps.
 DR InterPro; IPR009040; Ferritin_like.
 DR Pfam; PF00210; Ferritin; 1.
 DR PRINTS; PR00601; BACFERRITIN.

DR ProDom; PD002269; Bacterioferritin; 1.
 DR TIGRfam; TIGR00754; bfr; 1.
 DR PROSITE; PS00549; BACTERIOFERRITIN; 1.
 DR PROSITE; PS09005; FERRITIN LIKE; 1.
 KW Heme; Iron; Iron storage; Metal-binding.
 FT DOMAIN 1 147 Ferritin-like diiron.
 FT METAL 18 18 Iron 1 (By similarity).
 FT METAL 49 49 Iron (heme axial ligand) (Potential).
 FT METAL 51 51 Iron 1 (By similarity).
 FT METAL 51 51 Iron 2 (By similarity).
 FT METAL 54 54 Iron 1 (By similarity).
 FT METAL 94 94 Iron 2 (By similarity).
 FT METAL 129 129 Iron 1 (By similarity).
 FT METAL 129 129 Iron 2 (By similarity).
 FT METAL 132 132 Iron 2 (By similarity).
 SQ SEQUENCE 164 AA; 18491 MW; 6B837DCAFC72358 CRC64;
 Query Match 85.7%; Score 30; DB 1; Length 164;
 Best Local Similarity 83.3%; Pred. No. 1.4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DVSKRP 6
 Db 70 DVSKRP 75

Search completed: October 14, 2005, 16:19:57
 Job time : 48.5938 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2005, 15:51:19 ; Search time 84.5625 Seconds
(without alignments)
50.310 Million cell updates/sec

Title: US-10-614-959-15
Sequence: 1 AAWDLSLSEFL 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	11	3	AAV79073
2	58	100.0	104	2	AA80087 Human der
3	58	100.0	104	2	AAW95485 Human der
4	58	100.0	109	4	AAU02544 Anti-adip
5	58	100.0	110	4	AAU02558 Anti-adip
6	58	100.0	110	4	AAU02612 Anti-adip
7	58	100.0	110	4	AAU02627 Anti-adip
8	58	100.0	110	4	AAU02629 Anti-adip
9	58	100.0	111	2	AAW19883 CEA-speci
10	58	100.0	111	4	AAU02542 Anti-adip
11	58	100.0	111	4	AAU02551 Anti-adip
12	58	100.0	111	4	AAU02585 Anti-adip
13	58	100.0	111	4	AAU02606 Anti-adip
14	58	100.0	242	8	ADG34301 Neurokini
15	58	100.0	242	8	ADG34317 Neurokini
16	58	100.0	243	5	ABP45916 Human Bly
17	58	100.0	243	7	ADG96743 Single ch
18	58	100.0	243	8	ADG34310 Neurokini
19	58	100.0	243	8	ADG34306 Neurokini
20	58	100.0	244	5	ADG34303 Neurokini
21	58	100.0	245	5	ABP45915 Human Bly
22	58	100.0	245	7	ADG96742 Single ch
23	58	100.0	245	7	ADG98057 TNF proli
24	58	100.0	245	8	ADG83862 Chemokine
25	58	100.0	245	8	ADG34308 Neurokini

26	58	100.0	246	5	ABP45902 Human Bly
27	58	100.0	246	5	ABP45906 Human Bly
28	58	100.0	246	7	ADG96733 Single ch
29	58	100.0	246	7	ADG96729 Single ch
30	58	100.0	246	8	ADG83872 Chemokine
31	58	100.0	247	5	ABP45671 Human Bly
32	58	100.0	247	5	ABP45671 Human Bly
33	58	100.0	247	5	ABP45432 Human Bly
34	58	100.0	247	5	ABP45923 Human Bly
35	58	100.0	247	5	ABP45917 Human Bly
36	58	100.0	247	5	ABP45696 Human Bly
37	58	100.0	247	5	ABP45888 Human Bly
38	58	100.0	247	7	ADG30413 Human GMB
39	58	100.0	247	7	ADG30455 Human GMB
40	58	100.0	247	7	ADG96715 Single ch
41	58	100.0	247	7	ADG96498 Single ch
42	58	100.0	247	7	ADG96744 Single ch
43	58	100.0	247	7	ADG96259 Single ch
44	58	100.0	247	7	ADG96750 Single ch
45	58	100.0	247	7	ADG96523 Single ch
			247	8	ADG83874 Chemokine

ALIGNMENTS

RESULT 1
AAV79073
ID AAV79073 standard; peptide; 11 AA.
XX
AC AAV79073;
XX
DT 12-JUN-2000 . (first entry)
XX
DE Anti-factor IX/IXa antibody L chain V domain CDR3 amino acid sequence.
KW Complementarity determining region 3; CDR3; antibody; Gla domain;
KW factor IX/IXa; blood coagulation; deep venous thrombosis; light chain;
KW arterial thrombosis; unstable angina; post myocardial infarction;
KW coronary artery bypass graft; CABG; stroke; tumour growth; metastasis;
KW percutaneous transluminal coronary angioplasty; PTCA; inflammation;
KW septic shock; hypotension; adult respiratory distress syndrome; ARDS;
KW arterial fibrillation; disseminated intravascular coagulopathy; DIC.
OS Homo sapiens.
XX
PN WO200012562-A1.
XX
PD 09-MAR-2000.
XX
PF 26-AUG-1999; 99WO-US019453.
XX
PR 28-AUG-1998; 98US-0098233P.
XX
PR 03-MAR-1999; 99US-0122767P.
XX
PA (GETH) GENENTECH INC.
XX
PI Adams CW, Devaux B, Eaton DL, Haas PE, Judice JK, Kirchhofer D;
PI Suggett S;
XX
XX WPI; 2000-256595/22.
XX
PT Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-
PT carboxyglutamic acid domains useful as anti-coagulant in thrombosis,
XX stroke, and post myocardial infarction.
XX
PS Claim 8; Fig 2; 84pp; English.
XX
CC This sequence represents a complementarity determining region 3 (CDR3) of
CC the light chain variable domain of a human anti-factor IX/IXa Gla domain
CC antibody. Factor IXa is a vitamin K dependent plasma serine protease that
CC participates in the blood coagulation pathways. The Gla domain of factor
CC IXa and its zymogen factor IX contains important structural determinants
CC for interaction with high affinity binding sites on vascular endothelial

CCC	cells and platelets. Compositions comprising the antibodies are used for
CCC	the treatment or prophylaxis of thrombotic or coagulopathic diseases or
CCC	disorders in a mammal for which inhibiting a FIX/FIXa mediated event is
CCC	indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable
CCC	angina, post myocardial infarction, post surgical thrombosis, coronary
CCC	artery bypass graft (CABG), percutaneous transluminal coronary
CCC	angioplasty (PTCA), stroke, tumour growth, invasion or metastasis,
CCC	inflammation, septic shock, hypotension, adult respiratory distress
CCC	syndrome (ARDS), arterial fibrillation and disseminated intravascular
CCC	coagulopathy (DIC)
XX	
XX	
SSQ	Sequence 11 AA;
	Query Match 100.0%; Score 58; DB 3; Length 11;
	Best Local Similarity 100.0%; Pred. No. 0.0022;
	Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 AAWDDSLSEFL 11
DB	1 AAWDDSLSEFL 11
RESULT 2	
AAR80087	AAR80087 standard; protein; 104 AA.
ID	AAR80087 standard; protein; 104 AA.
XX	
AC	AAR80087;
XX	
DT	23-MAY-1996 (first entry)
XX	
DE	Human derived light chain RT3 phage antibody.
XX	
KW	Light chain; RT3; human; catalytic antibody; bacteriophage.
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	Region 7..15
FT	/note= "framework region 1"
FT	Region 16..28
FT	/note= "complementarity determining region 1"
FT	Region 29..42
FT	/note= "framework region 2"
FT	Region 43..50
FT	/note= "complementarity determining region 2"
FT	Region 51..82
FT	/note= "framework region 3"
FT	Region 83..93
FT	/note= "complementarity dtermining region 3"
FT	Region 94..104
FT	/note= "framework region 4"
XX	
PX	WO9527045-A1.
PN	
XX	
PD	12-OCT-1995.
XX	
PF	30-MAR-1994; 94WO-US003420.
XX	
PR	30-MAR-1994; 94WO-US003420.
XX	
PA	(IGEN-) IGEN INC.
XX	
PI	Smith RG, Mc Cafferty J, Chiswell D, Barsley MJ, Fitzgerald K;
PI	Kenten JH, Martin MT, Titmas RC, Williams RO;
XX	
DR	WPI; 1995-358624/46.
DR	N-PSDB; AAT04634.
XX	
PT	Production of catalytic antibodies displayed on phage - by generating a
PT	gene library of antibody-derived domains and expressing it in phage
PT	vectors.
XX	
PS	Disclosure; Fig 20; 133pp; English.

XX AAT04634 encodes AAR80087 human derived light chain RT3 phage antibody.
 CC The DNA was used in the prepn. of catalytic antibody (CA) producing
 CC bacteriophage. The CAs can be used to activate/deactivate a biological
 CC function in an animal by enhancing the rate of cleavage, or formation of
 CC a specific bond within a mol. in vivo
 XX
 XX SQ Sequence 104 AA;
 Query Match 100.0%; Score 58; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. NO. 0.023;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAWDDSLSEPL 11
 |||||
 DB 83 AAWDDSLSEPL 93
 RESULT 3
 AAW95485
 ID AAW95485 standard; protein; 104 AA.
 XX AC AAW95485;
 XX 29-MAR-1999 (first entry)
 XX Human-derived RT3 phage antibody light chain genetic sequence.
 XX Catalytic; antibody; phage display; immunising; phage expression vector;
 XX prodrug; scFV; RT3.
 XX Homo sapiens.
 XX OS
 XX US5855885-A.
 XX PN
 XX 05-JAN-1999.
 XX
 XX 14-JUL-1994; 94US-00273146.
 XX 22-JAN-1993; 93US-00007684.
 XX
 XX (MCCA/) MCCAFFERTY J.
 XX (CHIS/) CHISWELL D.
 XX (DARS/) DARSLEY M J.
 XX (TITM/) TITMAS R C.
 XX (MART/) MARTIN M T.
 XX (KENT/) KENTEN J H.
 XX (SMIT/) SMITH R.
 XX (FITZ/) FITZGERALD K.
 XX (WILL/) WILLIAMS R O.
 XX
 XX Fitzgerald K, Darsley MJ, Williams RO, Smith R, Martin MT;
 XX Kenten JH, Chiswell D, Mccafferty J, Titmas RC;
 XX
 XX WPI; 1999-105036/09.
 XX N-PSDB; AAX00884.
 XX
 XX Production of catalytic antibodies displayed on bacteriophages -
 XX comprises generating a gene library of antibody-derived domains inserting
 XX coding into a phage expression vector and isolating the catalytic
 XX antibodies.
 XX
 XX Example; Fig 20B; 117pp; English.
 XX
 XX The invention relates to methods for producing catalytic antibodies
 XX displayed on a phage. The method comprises: (a) generating a gene library
 XX of antibody-derived domains; (b) inserting coding for the domains into a
 XX phage expression vector; and (c) isolating the catalytic antibodies. The
 XX phage expression vector incorporates a histidine peptide in tandem with a
 XX myc peptide. The catalytic antibodies can be isolated by preparing an
 XX antigen; optionally immunising an animal with the antigen; generating a
 XX library of VH and VL domains from the immunised animal; cloning the VH
 XX and VL domains into a phage expression vector to generate phage display

CC antibodies; selecting phage display antibodies which bind specifically to
CC the antigen; screening the selected phage display antibodies for
CC catalytic activity to substrate; and isolating the catalytic antibodies,
CC where the phage expression vector incorporates a histidine peptide in
CC tandem with a myc peptide. The processes are used to produce catalytic
CC antibodies, which can be used for in vivo activation of a prodrug.
CC Sequences AA095484-489 represent genetic sequences of heavy and light
CC chains of RT3 specific phage antibodies selected from a naive human phage
CC antibody library

XX SQ Sequence 104 AA;

Query Match 100.0%; Score 58; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 0.023; 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0;

OY 1 AA02544
|||||
DB 83 AA02544

RESULT 4

AAU02544
ID AAU02544 standard; protein; 109 AA.

XX AC AAU02544;

DT 29-AUG-2001 (first entry)

XX DE Anti-adipocyte monoclonal antibody light chain, FAT 31.

XX KW Antibody; adipocyte; heavy chain; light chain; obesity; fat;
XX KW heart disease; complementarity determining region; CDR.

XX OS Homo sapiens.

XX FN WO200127279-A1.

XX PD 19-APR-2001.

XX PF 11-OCT-2000; 2000WO-GB003900.

XX PR 12-OCT-1999; 99US-0158812P.

XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX PI Edwards BM, Main SH, Vaughan TJ;

XX DR WPI; 2001-282031/29.

XX DR N-PSDB; RAS03444.

XX PT Panel of specific binding members of antibody molecules which bind to
XX PT whole adipocytes is used in the treatment of obesity and obesity related
XX PT diseases.

XX PS Claim 1; Page 120; 182pp; English.

XX CC AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
XX CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
XX CC and heavy chain complementarity determining regions (CDR) of the
XX CC invention. The antibodies can be used in the treatment of obesity and
XX CC obesity related diseases. The antibodies can be used to deliver drugs or
XX CC pro-drugs directly to the fat mass of an obese patient or the antibody
XX CC can be used as a therapeutic itself. Antibodies binding specifically to
XX CC adipocytes can be used to activate the immune system to destroy the cells
XX CC by complement mediated lysis. The antibodies may be labeled with a
XX CC detectable label such as radiolabel, fluorescent or chemical group and
XX CC used in methods of diagnosis in human subjects e.g. to determine the
XX CC presence of adipocyte antigen on the surface of an adipocyte to detect or
XX CC determine the presence or level of adipocytes in a cell or tissue sample.
XX CC The antibodies can be used as an alternative means of treatment for obese
XX CC patients other than undergoing surgery to remove excess fat. Antibodies
XX CC for different types of fat deposits can also be produced e.g. intra-

CC abdominal fat associated with heart disease
XX SQ Sequence 109 AA;

Query Match 100.0%; Score 58; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.024; 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0;

OY 1 AA02544
|||||
DB 90 AA02544

RESULT 5

AAU02558
ID AAU02558 standard; protein; 110 AA.

XX AC AAU02558;

DT 29-AUG-2001 (first entry)

XX DE Anti-adipocyte monoclonal antibody light chain, FAT 44.

XX KW Antibody; adipocyte; heavy chain; light chain; obesity; fat;
XX KW heart disease; complementarity determining region; CDR.

XX OS Homo sapiens.

XX FN WO200127279-A1.

XX PD 19-APR-2001.

XX PF 11-OCT-2000; 2000WO-GB003900.

XX PR 12-OCT-1999; 99US-0158812P.

XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX PI Edwards BM, Main SH, Vaughan TJ;

XX DR WPI; 2001-282031/29.

XX DR N-PSDB; RAS03458.

XX PT Panel of specific binding members of antibody molecules which bind to
XX PT whole adipocytes is used in the treatment of obesity and obesity related
XX PT diseases.

XX PS Claim 1; Page 128-129; 182pp; English.

XX CC AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
XX CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
XX CC and heavy chain complementarity determining regions (CDR) of the
XX CC invention. The antibodies can be used in the treatment of obesity and
XX CC obesity related diseases. The antibodies can be used to deliver drugs or
XX CC pro-drugs directly to the fat mass of an obese patient or the antibody
XX CC can be used as a therapeutic itself. Antibodies binding specifically to
XX CC adipocytes can be used to activate the immune system to destroy the cells
XX CC by complement mediated lysis. The antibodies may be labeled with a
XX CC detectable label such as radiolabel, fluorescent or chemical group and
XX CC used in methods of diagnosis in human subjects e.g. to determine the
XX CC presence of adipocyte antigen on the surface of an adipocyte to detect or
XX CC determine the presence or level of adipocytes in a cell or tissue sample.
XX CC The antibodies can be used as an alternative means of treatment for obese
XX CC patients other than undergoing surgery to remove excess fat. Antibodies
XX CC for different types of fat deposits can also be produced e.g. intra-

XX SQ Sequence 110 AA;

Query Match 100.0%; Score 58; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.024; 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0;

```

QY      1 AAWDDSLSEFL 11
Db      90 AAWDDSLSEFL 100

RESULT 6
AAU02612
ID AAU02612 standard; protein; 110 AA.
XX
AC
XX
DT
XX
XX
XX
DE Anti-adipocyte monoclonal antibody light chain, FAT 99.
XX
XX Antibody; adipocyte; heavy chain; light chain; obesity; fat;
KW heart disease; complementarity determining region; CDR.
XX
XX Homo sapiens.
XX
XX WO200127279-A1.
XX
XX 19-APR-2001.
XX
XX 11-OCT-2000; 2000WO-GB003900.
XX
XX 12-OCT-1999; 99US-0158812P.
XX
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Edwards BM, Main SH, Vaughan TJ;
XX
XX WPI; 2001-282031/29.
XX
XX N-PSDB; AAS03512.
XX
XX Panel of specific binding members of antibody molecules which bind to
PT whole adipocytes is used in the treatment of obesity and obesity related
PT diseases.
XX
XX Claim 1; Page 163; 182pp; English.
XX
XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
CC and heavy chain complementarity determining regions (CDR) of the
CC invention. The antibodies can be used in the treatment of obesity and
CC obesity related diseases. The antibodies can be used to deliver drugs or
CC pro-drugs directly to the fat mass of an obese patient or the antibody
CC can be used as a therapeutic itself. Antibodies binding specifically to
CC adipocytes can be used to activate the immune system to destroy the cells
CC by complement mediated lysis. The antibodies may be labeled with a
CC detectable label such as radiolabel, fluorescent or chemical group and
CC used in methods of diagnosis in human subjects e.g. to determine the
CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease
XX
XX Sequence 110 AA;
SQ
Query Match 100.0%; Score 58; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. NO. 0.024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AAWDDSLSEFL 11
Db      90 AAWDDSLSEFL 100

RESULT 7
AAU02627
ID AAU02627 standard; protein; 110 AA.

```

```

XX
AC AAU02627;
XX
XX 29-AUG-2001 (first entry)
XX
XX Anti-adipocyte monoclonal antibody light chain, FAT 112.
XX
XX Antibody; adipocyte; heavy chain; light chain; obesity; fat;
KW heart disease; complementarity determining region; CDR.
XX
XX Homo sapiens.
XX
XX WO200127279-A1.
XX
XX 19-APR-2001.
XX
XX 11-OCT-2000; 2000WO-GB003900.
XX
XX 12-OCT-1999; 99US-0158812P.
XX
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Edwards BM, Main SH, Vaughan TJ;
XX
XX WPI; 2001-282031/29.
XX
XX N-PSDB; AAS03527.
XX
XX Panel of specific binding members of antibody molecules which bind to
PT whole adipocytes is used in the treatment of obesity and obesity related
PT diseases.
XX
XX Claim 1; Page 172; 182pp; English.
XX
XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
CC and heavy chain complementarity determining regions (CDR) of the
CC invention. The antibodies can be used in the treatment of obesity and
CC obesity related diseases. The antibodies can be used to deliver drugs or
CC pro-drugs directly to the fat mass of an obese patient or the antibody
CC can be used as a therapeutic itself. Antibodies binding specifically to
CC adipocytes can be used to activate the immune system to destroy the cells
CC by complement mediated lysis. The antibodies may be labeled with a
CC detectable label such as radiolabel, fluorescent or chemical group and
CC used in methods of diagnosis in human subjects e.g. to determine the
CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease
XX
XX Sequence 110 AA;
SQ
Query Match 100.0%; Score 58; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. NO. 0.024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AAWDDSLSEFL 11
Db      90 AAWDDSLSEFL 100

RESULT 8
AAU02629
ID AAU02629 standard; protein; 110 AA.
XX
AC AAU02629;
XX
XX 29-AUG-2001 (first entry)
XX
XX Anti-adipocyte monoclonal antibody light chain, FAT 113.
XX
XX Antibody; adipocyte; heavy chain; light chain; obesity; fat;

```



```

XX 11-OCT-2000; 2000WO-GB003900.
XX
XX
PR 12-OCT-1999; 99US-0158812P.
XX
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Edwards BM, Main SH, Vaughan TJ;
XX
XX
XX WPI; 2001-282031/29.
XX N-PSDB; AAS03442.
XX
XX Panel of specific binding members of antibody molecules which bind to
XX whole adipocytes is used in the treatment of obesity and obesity related
XX diseases.
XX
XX Claim 1; Page 118-119; 182pp; English.
XX
XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
XX sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
XX and heavy chain complementarity determining regions (CDR) of the
XX invention. The antibodies can be used in the treatment of obesity and
XX obesity related diseases. The antibodies can be used to deliver drugs or
XX pro-drugs directly to the fat mass of an obese patient or the antibody
XX can be used as a therapeutic itself. Antibodies binding specifically to
XX adipocytes can be used to activate the immune system to destroy the cells
XX by complement mediated lysis. The antibodies may be labeled with a
XX detectable label such as radiolabel, fluorescent or chemical group and
XX used in methods of diagnosis in human subjects e.g. to determine the
XX presence of adipocyte antigen on the surface of an adipocyte to detect or
XX determine the presence or level of adipocytes in a cell or tissue sample.
XX The antibodies can be used as an alternative means of treatment for obese
XX patients other than undergoing surgery to remove excess fat. Antibodies
XX for different types of fat deposits can also be produced e.g. intra-
XX abdominal fat associated with heart disease
XX
XX SQ Sequence 111 AA;
XX
Query Match 100.0%; Score 58; DB 4; Length 111;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AAWDDSLSEFL 11
Db 90 AAWDDSLSEFL 100

RESULT 11
AAU02551
ID AAU02551 standard; protein; 111 AA.
XX
XX AAU02551;
XX
XX 29-AUG-2001 (first entry)
XX
XX Anti-adipocyte monoclonal antibody light chain, FAT 37.
XX
XX Antibody; adipocyte; heavy chain; light chain; obesity; fat;
XX heart disease; complementarity determining region; CDR.
XX
XX Homo sapiens.
XX
XX WO200127279-A1.
XX
XX 19-APR-2001.
XX
XX 11-OCT-2000; 2000WO-GB003900.
XX
XX 12-OCT-1999; 99US-0158812P.
XX
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Edwards BM, Main SH, Vaughan TJ;
XX

```

```

XX WPI; 2001-282031/29.
XX N-PSDB; AAS03451.
XX
XX Panel of specific binding members of antibody molecules which bind to
XX whole adipocytes is used in the treatment of obesity and obesity related
XX diseases.
XX
XX Claim 1; Page 124; 182pp; English.
XX
XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
XX sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
XX and heavy chain complementarity determining regions (CDR) of the
XX invention. The antibodies can be used in the treatment of obesity and
XX obesity related diseases. The antibodies can be used to deliver drugs or
XX pro-drugs directly to the fat mass of an obese patient or the antibody
XX can be used as a therapeutic itself. Antibodies binding specifically to
XX adipocytes can be used to activate the immune system to destroy the cells
XX by complement mediated lysis. The antibodies may be labeled with a
XX detectable label such as radiolabel, fluorescent or chemical group and
XX used in methods of diagnosis in human subjects e.g. to determine the
XX presence of adipocyte antigen on the surface of an adipocyte to detect or
XX determine the presence or level of adipocytes in a cell or tissue sample.
XX The antibodies can be used as an alternative means of treatment for obese
XX patients other than undergoing surgery to remove excess fat. Antibodies
XX for different types of fat deposits can also be produced e.g. intra-
XX abdominal fat associated with heart disease
XX
XX SQ Sequence 111 AA;
XX
Query Match 100.0%; Score 58; DB 4; Length 111;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AAWDDSLSEFL 11
Db 91 AAWDDSLSEFL 101

RESULT 12
AAU02585
ID AAU02585 standard; protein; 111 AA.
XX
XX AAU02585;
XX
XX 29-AUG-2001 (first entry)
XX
XX Anti-adipocyte monoclonal antibody light chain, FAT 72.
XX
XX Antibody; adipocyte; heavy chain; light chain; obesity; fat;
XX heart disease; complementarity determining region; CDR.
XX
XX Homo sapiens.
XX
XX WO200127279-A1.
XX
XX 19-APR-2001.
XX
XX 11-OCT-2000; 2000WO-GB003900.
XX
XX 12-OCT-1999; 99US-0158812P.
XX
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Edwards BM, Main SH, Vaughan TJ;
XX
XX WPI; 2001-282031/29.
XX N-PSDB; AAS03485.
XX
XX Panel of specific binding members of antibody molecules which bind to
XX whole adipocytes is used in the treatment of obesity and obesity related
XX diseases.
XX

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Db 221 AAWDDSLSEFL 231

RESULT 15

ADG34317
ID ADG34317 standard; protein; 242 AA.

XX AC ADG34317;

XX DT 26-FEB-2004 (first entry)

XX DE Neurokinin B antibody SEQ ID NO:40.

XX KW antibody; neurokinin B; hypotensive; gynaecological; gene therapy;

XX KW hypertension; pre-eclampsia; NKB.

XX OS Synthetic.

XX PN WO2003102136-A2.

XX PD 11-DEC-2003.

XX PF 29-MAY-2003; 2003WO-US016802.

XX PR 30-MAY-2002; 2002US-0383802P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Rosen CA, Ruben SM;

XX DR WPI; 2004-053456/05.

XX DR N-PSDB; ADG34298.

XX PT New antibody that specifically binds neurokinin B, useful for preparing a

XX PS composition for treating or preventing hypertension or preeclampsia.

XX SQ Claim 2; SEQ ID NO 40; 127pp; English.

XX CC The invention relates to a novel antibody specifically binding neurokinin

XX CC B. An antibody of the invention has hypotensive, and gynaecological

XX CC activity, and may have a use in gene therapy. The antibody is useful for

XX CC preparing a composition for treating or preventing hypertension or pre-

XX CC eclampsia. The present sequence is used in the exemplification of the

XX CC invention.

XX SQ Sequence 242 AA;

Query Match 100.0%; Score 58; DB 8; Length 242;

Best Local Similarity 100.0%; Pred. No. 0.056;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAWDDSLSEFL 11

|||||

Db 221 AAWDDSLSEFL 231

Search completed: October 14, 2005, 16:12:42

Job time : 84.5625 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2005, 16:00:04 ; Search time 21.6562 Seconds
(without alignments)
37.917 Million cell updates/sec

Title: US-10-614-959-15
Perfect score: 58
Sequence: 1 AAWDDSLSEFL 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	11	4	US-09-383-667-15
2	58	100.0	104	2	Sequence 15, Appl
3	58	100.0	111	2	Sequence 63, Appl
4	46	79.3	11	2	Sequence 15, Appl
5	46	79.3	11	2	Sequence 374, Appl
6	44	75.9	11	2	Sequence 346, Appl
7	44	75.9	11	4	Sequence 346, Appl
8	43	74.1	9	2	Sequence 60, Appl
9	43	74.1	9	4	Sequence 60, Appl
10	43	74.1	10	2	Sequence 339, Appl
11	43	74.1	10	2	Sequence 497, Appl
12	43	74.1	10	4	Sequence 339, Appl
13	43	74.1	10	4	Sequence 497, Appl
14	43	74.1	11	2	Sequence 441, Appl
15	43	74.1	11	2	Sequence 441, Appl
16	43	74.1	11	2	Sequence 6, Appl
17	43	74.1	11	4	Sequence 441, Appl
18	43	74.1	98	2	Sequence 6, Appl
19	43	74.1	98	2	Sequence 111, Appl
20	43	74.1	98	4	Sequence 38, Appl
21	43	74.1	109	3	Sequence 58, Appl
22	43	74.1	110	3	Sequence 60, Appl
23	43	74.1	111	2	Sequence 36, Appl
24	43	74.1	111	2	Sequence 36, Appl
25	43	74.1	111	4	Sequence 43, Appl
26	43	74.1	111	4	Sequence 36, Appl
27	43	74.1	112	2	Sequence 39, Appl

US-09-383-667-15
; Sequence 15, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camelia W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Eaton, Dan L.
; APPLICANT: Hass, Phillip E.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Kirchofer, Daniel
; APPLICANT: Suggett, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: P1661R2
; CURRENT APPLICATION NUMBER: US/09/383.667
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098.233
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: US 60/122.767
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 15
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-667-15
Query Match 100.0%; Score 58; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 11, Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAWDDSLSEFL 11
Db 1 AAWDDSLSEFL 11
RESULT 2
US-08-273-146-63
; Sequence 63, Application US/08273146
; Patent No. 5855885
; GENERAL INFORMATION:
; APPLICANT: Smith, Rodger
; APPLICANT: McCafferty, John
; APPLICANT: Chiswell, David
; APPLICANT: Darsley, Michael J.
; APPLICANT: Fitzgerald, Kevin
; APPLICANT: Kenten, John H.
; APPLICANT: Martin, Mark T.
; APPLICANT: Timas, Richard C.
; APPLICANT: Williams, Richard O.

ALIGNMENTS

RESULT 1
US-09-383-667-15
; Sequence 15, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camelia W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Eaton, Dan L.
; APPLICANT: Hass, Phillip E.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Kirchofer, Daniel
; APPLICANT: Suggett, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: P1661R2
; CURRENT APPLICATION NUMBER: US/09/383.667
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098.233
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: US 60/122.767
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 15
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-667-15
Query Match 100.0%; Score 58; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 11, Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAWDDSLSEFL 11
Db 1 AAWDDSLSEFL 11
RESULT 2
US-08-273-146-63
; Sequence 63, Application US/08273146
; Patent No. 5855885
; GENERAL INFORMATION:
; APPLICANT: Smith, Rodger
; APPLICANT: McCafferty, John
; APPLICANT: Chiswell, David
; APPLICANT: Darsley, Michael J.
; APPLICANT: Fitzgerald, Kevin
; APPLICANT: Kenten, John H.
; APPLICANT: Martin, Mark T.
; APPLICANT: Timas, Richard C.
; APPLICANT: Williams, Richard O.

;
; TITLE OF INVENTION: The Isolation and Production of
; TITLE OF INVENTION: Catalytic Antibodies using Phage Technology
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IGEN, Inc.
; STREET: 1530 East Jefferson St.
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20852
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/273,146
; APPLICATION NUMBER: US/08/273,146
; FILING DATE: 14-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ryan, John W.
; REGISTRATION NUMBER: 33,771
; REFERENCE/DOCKET NUMBER: 09000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-984-8000
; TELEFAX: 301-230-0158
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-273-146-63

Query Match 100.0%; Score 58; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAWDDSLSEFL 11
Db 83 AAWDDSLSEFL 93

RESULT 3
US-08-652-816A-15
; Sequence 15, Application US/08652816A
; Patent No. 5872215
; GENERAL INFORMATION:
; APPLICANT: Osbourn, JK
; APPLICANT: Allen, DJ
; APPLICANT: McCafferty, JG
; TITLE OF INVENTION: Specific binding members, materials and
; TITLE OF INVENTION: Methods.
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,816A
; FILING DATE: 23-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9125579.4
; FILING DATE: 02-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9125579.8

;
; FILING DATE: 02-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206372.6
; FILING DATE: 23-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9525004.9
; FILING DATE: 07-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9610824.6
; FILING DATE: 23-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/02240
; FILING DATE: 02-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/244,597
; FILING DATE: 01-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/33308
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-652-816A-15

Query Match 100.0%; Score 58; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAWDDSLSEFL 11
Db 90 AAWDDSLSEFL 100

RESULT 4
US-08-350-260A-374
; Sequence 374, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; TITLE OF INVENTION: binding pairs
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435

APPLICATION NUMBER: US/09/104,337A
FILING DATE: 25-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/350,260
FILING DATE: 05-DEC-1994
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bartnicki, Audrey L.
REGISTRATION NUMBER: 40,499
REFERENCE/DOCKET NUMBER: 28111/32372A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 374:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 374:
US-09-104-337A-374

Query Match 79.3%; Score 46; DB 4; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.05;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAWDDSLSEFL 11
Db 1 AAWDDSLSAV 11

RESULT 6
US-08-350-260A-346
Sequence 346, Application US/08350260A
Patent No. 5962255
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
APPLICANT: Griffiths, Andrew David
APPLICANT: Williams, Samuel Cameron
APPLICANT: Waterhouse, Peter
APPLICANT: Nissim, Ahuva
APPLICANT: Johnson, Kevin Stuart
APPLICANT: Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
NUMBER OF SEQUENCES: 602
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough
STREET: Marshall, O'Toole, Gerstein, Murray & Borun
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,260A
FILING DATE: 05-DEC-1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
APPLICATION NUMBER: PCT/GB91/01134
FILING DATE: 10-JUL-1991
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/32372
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 374:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-350-260A-374

Query Match 79.3%; Score 46; DB 2; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.05;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAWDDSLSEFL 11
Db 1 AAWDDSLSAV 11

RESULT 5
US-09-104-337A-374
Sequence 374, Application US/09104337A
Patent No. 6492160
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
APPLICANT: Griffiths, Andrew David
APPLICANT: Williams, Samuel Cameron
APPLICANT: Waterhouse, Peter
APPLICANT: Nissim, Ahuva
APPLICANT: Johnson, Kevin Stuart
APPLICANT: Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
binding pairs
NUMBER OF SEQUENCES: 600
CORRESPONDENCE ADDRESS:
ADDRESSEE: Audrey L. Bartnicki
STREET: Marshall, Gerstein & Borun
3300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bartnicki, Audrey L.
; REGISTRATION NUMBER: 40,499
; REFERENCE/DOCKET NUMBER: 28111/32372A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 346:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 346:
US-08-350-260A-346

Query Match 75.9%; Score 44; DB 2; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.11;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAWDDSLSEFL 11
Db 1 AAWDDSLAWFV 11

RESULT 7
US-09-104-337A-346
; Sequence 346, Application US/09104337A
; Patent No. 6492160
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; Griffiths, Andrew David
; Williams, Samuel Cameron
; Waterhouse, Peter
; Nissim, Ahuva
; Johnson, Kevin Stuart
; Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; binding pairs
; NUMBER OF SEQUENCES: 600
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Audrey L. Bartnicki
; STREET: Marshall, Gerstein & Borun
; 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/350,260
; FILING DATE: 05-DEC-1994
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 24-MAR-1992
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bartnicki, Audrey L.
; REGISTRATION NUMBER: 40,499
; REFERENCE/DOCKET NUMBER: 28111/32372A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 346:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 346:
US-09-104-337A-346

Query Match 75.9%; Score 44; DB 4; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.11;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAWDDSLSEFL 11
Db 1 AAWDDSLAWFV 11

RESULT 8
US-08-665-202-60
; Sequence 60, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,202
; FILING DATE: 13-JUN-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
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LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-350-260A-339

Query Match 74.1%; Score 43; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDSLS 8
Db 1 AAWDSLS 8

RESULT 11

US-08-350-260A-497
Sequence 497, Application US/08350260A
Patent No. 5962255
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
APPLICANT: Griffiths, Andrew David
APPLICANT: Williams, Samuel Cameron
APPLICANT: Waterhouse, Peter
APPLICANT: Nissim, Ahuva
APPLICANT: Johnson, Kevin Stuart
APPLICANT: Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
binding pairs
NUMBER OF SEQUENCES: 602
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough
STREET: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350.260A
FILING DATE: 05-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB91/01134
FILING DATE: 10-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/32372
TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 497:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-350-260A-497

Query Match 74.1%; Score 43; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDSLS 8
Db 1 AAWDSLS 8

RESULT 12

US-09-104-337A-339
Sequence 339, Application US/09104337A
Patent No. 6492160
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
APPLICANT: Griffiths, Andrew David
APPLICANT: Williams, Samuel Cameron
APPLICANT: Waterhouse, Peter
APPLICANT: Nissim, Ahuva
APPLICANT: Johnson, Kevin Stuart
APPLICANT: Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
binding pairs
NUMBER OF SEQUENCES: 600
CORRESPONDENCE ADDRESS:
ADDRESSEE: Audrey L. Bartnicki
STREET: Marshall, Gerstein & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104.337A
FILING DATE: 25-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/350,260
FILING DATE: 05-DEC-1994
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bartnicki, Audrey L.
REGISTRATION NUMBER: 40,499
REFERENCE/DOCKET NUMBER: 28111/32372A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 339:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids

Job time : 21.6562 secs

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; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-350-260A-441

Query Match 74.1%; Score 43; DB 2; Length 11;
Best Local Similarity 100.0%; Pred.No. 0.17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAWDDSL 8
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Db 1 AAWDDSL 8

RESULT 15

US-08-665-202-6
; Sequence 6, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,202
; FILING DATE: 13-JUN-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061410
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-665-202-6

Query Match 74.1%; Score 43; DB 2; Length 11;
Best Local Similarity 100.0%; Pred.No. 0.17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAWDDSL 8
| | | | |
Db 1 AAWDDSL 8

Search completed: October 14, 2005, 16:22:03

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OM protein - protein search, using sw model

Run on: October 14, 2005, 16:20:10 ; Search time 78.2031 Seconds
(without alignments)
58.615 Million cell updates/sec

Title: US-10-614-959-15
Perfect score: 58
Sequence: 1 AAWDDSLSEFL 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1859788 seqs, 416717961 residues

Total number of hits satisfying chosen parameters: 1859789

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
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19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	242	18	US-10-981-692-24
2	58	100.0	242	18	US-10-981-692-40
3	58	100.0	243	10	US-09-880-748-1927
4	58	100.0	243	15	US-10-293-418-1927
5	58	100.0	243	18	US-10-981-692-29
6	58	100.0	243	18	US-10-981-692-33
7	58	100.0	244	18	US-10-981-692-26
8	58	100.0	245	10	US-09-880-748-1926
9	58	100.0	245	15	US-10-293-418-1926
10	58	100.0	245	15	US-10-293-418-3241
11	58	100.0	245	18	US-10-981-692-31

12	58	100.0	246	10	US-09-880-748-1913	Sequence 1913, Ap
13	58	100.0	246	10	US-09-880-748-1917	Sequence 1917, Ap
14	58	100.0	246	15	US-10-293-418-1913	Sequence 1913, Ap
15	58	100.0	246	15	US-10-293-418-1917	Sequence 1917, Ap
16	58	100.0	247	10	US-09-880-748-1443	Sequence 1443, Ap
17	58	100.0	247	10	US-09-880-748-1682	Sequence 1682, Ap
18	58	100.0	247	10	US-09-880-748-1707	Sequence 1707, Ap
19	58	100.0	247	10	US-09-880-748-1899	Sequence 1899, Ap
20	58	100.0	247	10	US-09-880-748-1928	Sequence 1928, Ap
21	58	100.0	247	10	US-09-880-748-1934	Sequence 1934, Ap
22	58	100.0	247	15	US-10-293-418-1443	Sequence 1443, Ap
23	58	100.0	247	15	US-10-293-418-1682	Sequence 1682, Ap
24	58	100.0	247	15	US-10-293-418-1707	Sequence 1707, Ap
25	58	100.0	247	15	US-10-293-418-1899	Sequence 1899, Ap
26	58	100.0	247	15	US-10-293-418-1928	Sequence 1928, Ap
27	58	100.0	247	15	US-10-293-418-1934	Sequence 1934, Ap
28	58	100.0	247	17	US-10-935-290-46	Sequence 46, Appl
29	58	100.0	247	17	US-10-935-290-88	Sequence 88, Appl
30	58	100.0	247	18	US-10-981-692-27	Sequence 27, Appl
31	58	100.0	247	18	US-10-981-692-37	Sequence 37, Appl
32	58	100.0	247	20	US-11-046-857-44	Sequence 44, Appl
33	58	100.0	248	18	US-10-981-692-39	Sequence 39, Appl
34	58	100.0	249	10	US-09-880-748-1419	Sequence 1419, Ap
35	58	100.0	249	10	US-09-880-748-1618	Sequence 1618, Ap
36	58	100.0	249	10	US-09-880-748-2049	Sequence 2049, Ap
37	58	100.0	249	10	US-09-880-748-2065	Sequence 2065, Ap
38	58	100.0	249	15	US-10-293-418-1419	Sequence 1419, Ap
39	58	100.0	249	15	US-10-293-418-1618	Sequence 1618, Ap
40	58	100.0	249	15	US-10-293-418-2049	Sequence 2049, Ap
41	58	100.0	249	15	US-10-293-418-2065	Sequence 2065, Ap
42	58	100.0	249	20	US-11-017-030-14	Sequence 14, Appl
43	58	100.0	250	18	US-10-981-692-22	Sequence 22, Appl
44	58	100.0	250	20	US-11-090-847-84	Sequence 84, Appl
45	58	100.0	251	10	US-09-880-748-1309	Sequence 1309, Ap

ALIGNMENTS

RESULT 1
US-10-981-692-24
; Sequence 24, Application US/10981692
; Publication No. US20050163777A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
; FILE REFERENCE: PF590P1
; CURRENT APPLICATION NUMBER: US/10/981,692
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: PCT/US03/16802
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/383,802
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: N015E08 scFv
US-10-981-692-24

Query Match 100.0% Score 58; DB 18; Length 242;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAWDDSLSEFL 11
Db 221 AAWDDSLSEFL 231
RESULT 2

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US-10-981-692-40
; Sequence 40, Application US/10981692
; Publication No. US20050163777A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
; CURRENT APPLICATION NUMBER: US/10/981,692
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: PCT/US03/16802
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/383,802
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: N015D10 scFv
US-10-981-692-40

Query Match      100.0%; Score 58; DB 18; Length 242;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AAWDDSLSEFL 11
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Db      221 AAWDDSLSEFL 231

RESULT 3
US-09-880-748-1927
; Sequence 1927, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1927
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1927

Query Match      100.0%; Score 58; DB 10; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AAWDDSLSEFL 11
      |||||
Db      222 AAWDDSLSEFL 232

RESULT 4
US-10-293-418-1927
; Sequence 1927, Application US/10293418
; Publication No. US20030223996A1
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US-10-981-692-29
; Sequence 29, Application US/10981692
; Publication No. US20050163777A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
; FILE REFERENCE: PF590P1
; CURRENT APPLICATION NUMBER: US/10/981,692
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: PCT/US03/16802
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/383,802
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: N024E07 scFv
US-10-981-692-29

Query Match      100.0%; Score 58; DB 18; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AAWDDSLSEFL 11
      |||||
Db      222 AAWDDSLSEFL 232

RESULT 5
US-10-981-692-29
; Sequence 29, Application US/10981692
; Publication No. US20050163777A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
; FILE REFERENCE: PF590P1
; CURRENT APPLICATION NUMBER: US/10/981,692
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: PCT/US03/16802
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/383,802
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: N024E07 scFv
US-10-981-692-29

Query Match      100.0%; Score 58; DB 18; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AAWDDSLSEFL 11
      |||||
Db      222 AAWDDSLSEFL 232

RESULT 6
US-10-981-692-33
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; Sequence 33, Application US/10981692
; Publication No. US20050163777A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
; FILE REFERENCE: PF590P1
; CURRENT APPLICATION NUMBER: US/10/981,692
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: PCT/US03/16802
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/383,802
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: N023E01 scFv
US-10-981-692-33

Query Match      100.0%; Score 58; DB 18; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AAWDDSLSEFL 11
Db      222 AAWDDSLSEFL 232

RESULT 7
US-10-981-692-26
; Sequence 26, Application US/10981692
; Publication No. US20050163777A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
; FILE REFERENCE: PF590P1
; CURRENT APPLICATION NUMBER: US/10/981,692
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: PCT/US03/16802
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/383,802
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: N024D01 scFv
US-10-981-692-26

Query Match      100.0%; Score 58; DB 18; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AAWDDSLSEFL 11
Db      223 AAWDDSLSEFL 233

RESULT 8
US-09-880-748-1926
; Sequence 1926, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
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; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1926
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1926

Query Match      100.0%; Score 58; DB 10; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AAWDDSLSEFL 11
Db      224 AAWDDSLSEFL 234

RESULT 9
US-10-293-418-1926
; Sequence 1926, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1926
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1926

Query Match      100.0%; Score 58; DB 15; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AAWDDSLSEFL 11
Db      224 AAWDDSLSEFL 234

RESULT 10
US-10-293-418-3241
; Sequence 3241, Application US/10293418
```

; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3241
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-3241

Query Match 100.0%; Score 58; DB 15; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAWDDSLSEFL 11
| | | | | | | | | | |
Db 224 AAWDDSLSEFL 234

RESULT 11
US-10-981-692-31
; Sequence 31, Application US/10981692
; Publication No. US20050163777A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
; FILE REFERENCE: PF590P1
; CURRENT APPLICATION NUMBER: US/10/981,692
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: PCT/US03/16802
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/383,802
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: N024D08 scFV
US-10-981-692-31

Query Match 100.0%; Score 58; DB 18; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAWDDSLSEFL 11
| | | | | | | | | | |
Db 224 AAWDDSLSEFL 234

RESULT 12

US-09-880-748-1913
; Sequence 1913, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1913
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1913

Query Match 100.0%; Score 58; DB 10; Length 246;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAWDDSLSEFL 11
| | | | | | | | | | |
Db 225 AAWDDSLSEFL 235

RESULT 13
US-09-880-748-1917
; Sequence 1917, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1917
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1917

Query Match 100.0%; Score 58; DB 10; Length 246;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAWDDSLSEFL 11
| | | | | | | | | | |
Db 225 AAWDDSLSEFL 235

US-10-293-418-1917

Query Match 100.0%; Score 58; DB 15; Length 246;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAWDDSLSEFL 11
Db 225 AAWDDSLSEFL 235

Search completed: October 14, 2005, 17:00:44
Job time : 78.2031 secs

RESULT 14

US-10-293-418-1913

; Sequence 1913, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1913
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-293-418-1913

Query Match 100.0%; Score 58; DB 15; Length 246;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAWDDSLSEFL 11
Db 225 AAWDDSLSEFL 235

RESULT 15

US-10-293-418-1917

; Sequence 1917, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
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; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1917
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo sapiens

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OM protein - protein search, using sw model

Run on: October 14, 2005, 16:02:59 ; Search time 15.2969 Seconds
(without alignments)
69.190 Million cell updates/sec

Title: US-10-614-959-15
Perfect score: 58
Sequence: 1 AAWDDSLSEFL 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	74.1	98	2 S36048	Ig lambda chain -
2	43	74.1	129	2 S78058	Ig lambda chain pr
3	43	74.1	235	2 S25750	Ig lambda chain -
4	41	70.7	112	1 LIHUMM	Ig lambda chain V-
5	40	69.0	95	2 S49571	Ig lambda chain pr
6	40	69.0	98	2 S36047	Ig lambda chain -
7	40	69.0	98	2 S36046	Ig lambda chain -
8	40	69.0	109	1 LIHUMA	Ig lambda chain V-
9	40	69.0	117	2 S23627	Ig lambda chain pr
10	40	69.0	149	2 S23626	Ig lambda chain V
11	40	69.0	233	2 S25752	Ig lambda chain -
12	40	69.0	234	2 S25757	Ig lambda chain -
13	40	69.0	235	2 S25754	Ig lambda chain -
14	40	69.0	355	2 E87394	conserved hypotet
15	40	69.0	497	2 G95983	probable glycerol
16	40	69.0	502	2 S49113	hypothetical prote
17	40	69.0	4367	1 B54802	dynein heavy chain
18	39	67.2	110	2 S57428	Ig light chain V-J
19	39	67.2	112	2 D44151	Ig lambda chain V
20	39	67.2	130	2 S78057	Ig lambda chain pr
21	39	67.2	397	1 OKB082	protein kinase (EC
22	39	67.2	1995	2 T08166	probable membrane
23	39	67.2	4344	1 A53489	dynein heavy chain
24	38	65.5	210	2 GB4751	hypothetical prote
25	38	65.5	329	2 T18622	hypothetical prote
26	38	65.5	423	2 S41289	hypothetical prote
27	38	65.5	443	2 T30619	probable serine/th
28	38	65.5	842	2 B55853	outer membrane ush
29	38	65.5	885	1 WMBY3L	ribonucleoside-dip

30 37.5 64.7 166 2 C83366 hypothetical prote
31 37 63.8 259 2 T40104 conserved hypotet
32 37 63.8 371 2 AH0147 outer membrane pro
33 37 63.8 395 2 T40102 conserved hypotet
34 37 63.8 476 2 H84228 thiamin biosynthes
35 37 63.8 644 2 F84698 probable thiamin b
36 37 63.8 655 2 A70931 probable PPE prote
37 37 63.8 857 2 B63798 hypothetical prote
38 37 63.8 1485 2 S23756 hypothetical prote
39 36 62.1 184 1 IVHOA1 CFR protein - Afr
40 36 62.1 184 1 IVHOA2 interferon alpha-I
41 36 62.1 184 1 IVHOA3 interferon alpha-I
42 36 62.1 184 1 IVHOA4 interferon alpha-I
43 36 62.1 227 2 F81855 interferon alpha-I
44 36 62.1 280 2 C98208 insertion element
45 36 62.1 280 2 AF3078 probable sugar tra
hypothetical prote

ALIGNMENTS

RESULT 1
S36048
Ig lambda chain - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C:Accession: S36048; S36049
R:Williams, S.C.
submitted to the EMBL Data Library, April 1993
A:Reference number: S36046
A:Accession: S36048
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <WIL>
A:Cross-references: EMBL:Z22189; NID:G312294; PIDN:CAA80199.1; PID:G312295; EMBL:Z22190
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-91/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 43; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAWDDSLS 8
Db 90 AAWDDSLS 97

RESULT 2
S78058
Ig lambda chain precursor V-J region (clone mAB 67VL) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C:Accession: S78058; S23723
R:Harindranath, N.
submitted to the EMBL Data Library, August 1990
A:Reference number: S78051
A:Accession: S78058
A:Molecule type: mRNA
A:Residues: 1-129 <HAR>
A:Cross-references: EMBL:X54446; NID:G37923; PIDN:CAA38313.1; PID:G930121
R:Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins, R.
Int. Immunol. 3, 865-875, 1991
A:Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and hi patient.
A:Reference number: S23716; MUID:92031262; PMID:1718404
A:Accession: S23723
A:Molecule type: mRNA
A:Residues: 19-129 <HAW>
A:Cross-references: EMBL:X54446
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-18/Domain: signal sequence (fragment) #status predicted <SIG>

F;19-129/Product: Ig lambda chain (fragment) #status predicted <MAT>
F;33-109/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 43; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDDSL 8

DB 108 AAWDDSL 115

RESULT 3

S25750
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25750
R;Combratio, G.; Klobbeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lambda
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25750
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-235 <COM>
A;Cross-references: EMBL:X57815; NID:G33729; PIDN:CAA40952.1; PID:G33730
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;150-218/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 43; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDDSL 8

DB 109 AAWDDSL 116

RESULT 4

LiHUMM
Ig lambda chain V-I region (Mem) - human
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C;Accession: A25479
R;Mihaesco, E.; Roy, J.P.; Congy, N.; Peran-Rivat, L.; Mihaesco, C.
Eur. J. Biochem. 150, 349-357, 1985
A;Title: The amino acid sequence of a lambda light chain presenting abnormal physicochem
A;Reference number: A25479; MUID:85257662; PMID:2410269
A;Accession: A25479
A;Molecule type: protein
A;Residues: 1-112 <MIH>
A;Cross-references: UNIPROT:P06987
A;Note: residues 33-36 and some of the sequenced peptides were positioned by homology
C;Comment: The C region of this chain has the Mcg+ and Kern+ markers.
C;Genetics:
A;Gene: GDB:IGLV@

A;Cross-references: GDB:119342; OMIM:147240
A;Map position: 22q11.2-22q11.2
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as Iga and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin; pyroglutamic acid
F;15-92/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;22-90/Disulfide bonds: #status predicted

Query Match 70.7%; Score 41; DB 1; Length 112;
Best Local Similarity 63.6%; Pred. No. 3.4;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAWDDSLSEFL 11

DB 91 AAWDDSLDGYV 101

RESULT 5

S49571
Ig lambda chain precursor V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 05-Mar-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
C;Accession: S49571
R;Giachino, C.; Padovan, E.; Lanzavecchia, A.
submitted to the EMBL Data Library, November 1994
A;Description: k+1+ dual receptor B cells are present in the human peripheral repertoire.
A;Reference number: S49571
A;Accession: S49571
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-95 <GTA>
A;Cross-references: EMBL:Z46625; NID:G575259; PIDN:CAA86595.1; PID:G575260
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 69.0%; Score 40; DB 2; Length 95;
Best Local Similarity 87.5%; Pred. No. 4.2;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDDSL 8

DB 76 AAWDDSLT 83

RESULT 6

S36047
Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C;Accession: S36047
R;Williams, S.C.
submitted to the EMBL Data Library, April 1993
A;Reference number: S36046
A;Accession: S36047
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <WIL>
A;Cross-references: EMBL:Z22188; NID:G312291; PIDN:CAA80198.1; PID:G312292
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-91/Domain: immunoglobulin homology <IMM>

Query Match 69.0%; Score 40; DB 2; Length 98;
Best Local Similarity 87.5%; Pred. No. 4.4;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDDSL 8

DB 90 AAWDDSLN 97

RESULT 7

S36046
Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S36046
R;Williams, S.C.
submitted to the EMBL Data Library, April 1993
A;Reference number: S36046
A;Accession: S36046
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <WIL>
A;Cross-references: EMBL:Z22187; NID:G312312; PIDN:CAA80197.1; PID:G312313
C;Superfamily: immunoglobulin V region; immunoglobulin homology

```
C;Keywords: heterotetramer; immunoglobulin

Query Match      69.0%; Score 40; DB 2; Length 98;
Best Local Similarity 87.5%; Pred. No. 4.4;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AAWDDSL 8
Db 90 AAWDDSLN 97

RESULT 8
LIHWA
Ig lambda chain V-I region (Wah) - human
C;Species: Homo sapiens (man)
C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004
C;Accession: A01967
R;Takahashi, Y.; Takahashi, N.; Tetaert, D.; Putnam, F.W.
Proc. Natl. Acad. Sci. U.S.A. 80, 3686-3690, 1983
A;Title: Complete covalent structure of a human immunoglobulin D: sequence of the lambda
A;Reference number: A01967; MUID:83221661; PMID:6407018
A;Accession: A01967
A;Molecule type: protein
A;Residues: 1-109 <TAK>
A;Cross-references: UNIPROT:P04208
C;Genetics:
A;Gene: GDB:IGLV@
A;Cross-references: GDB:119342; OMIM:147240
A;Map position: 22q11.2-22q11.2
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-97/Region: V segment
F;15-91/Domain: immunoglobulin homology <IMM>
F;98-109/Region: J segment
F;22-89/Disulfide bonds: #status predicted

Query Match      69.0%; Score 40; DB 1; Length 109;
Best Local Similarity 80.0%; Pred. No. 4.9;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 AAWDDSLSEF 10
Db 90 AAWDDSLVWF 99

RESULT 9
Ig lambda chain precursor - human
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S23627
R;Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.;
J. Exp. Med. 175, 831-842, 1992
A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from t
A;Reference number: S23623; MUID:92156804; PMID:1740665
A;Accession: S23627
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-117 <OLE>
A;Cross-references: EMBL:X59707; NID:G34426; PIDN:CAA42228.1; PID:G34427
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-110/Domain: immunoglobulin homology <IMM>

Query Match      69.0%; Score 40; DB 2; Length 117;
Best Local Similarity 87.5%; Pred. No. 5.3;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 AAWDDSL 8
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C;Keywords: heterotetramer; immunoglobulin

Query Match      69.0%; Score 40; DB 2; Length 149;
Best Local Similarity 87.5%; Pred. No. 6.9;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AAWDDSL 8
Db 109 AAWDDSLN 116

RESULT 10
Ig lambda chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S23626
R;Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.;
J. Exp. Med. 175, 831-842, 1992
A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from tv
A;Reference number: S23623; MUID:92156804; PMID:1740665
A;Accession: S23626
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-149 <OLS>
A;Cross-references: EMBL:X59706; NID:G34204; PIDN:CAA42227.1; PID:G34205
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-110/Domain: immunoglobulin homology <IMM>

Query Match      69.0%; Score 40; DB 2; Length 233;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AAWDDSL 8
Db 107 AAWDDSLN 114

RESULT 12
Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25757
R;Combrato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25757
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-233 <COM>
A;Cross-references: EMBL:X57817; NID:G33733; PIDN:CAA40954.1; PID:G33734
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;148-216/Domain: immunoglobulin homology <IMM>

Query Match      69.0%; Score 40; DB 2; Length 233;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AAWDDSL 8
Db 107 AAWDDSLN 114

RESULT 12
Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25757
R;Combrato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25757
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
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A;Residues: 1-234 <COM>
 A;Cross-references: EMBL:X57822; NID:g33743; PIDN:CAA40959.1; PID:g33744
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;149-217/Domain: immunoglobulin homology <IMM>

Query Match 69.0%; Score 40; DB 2; Length 234;
 Best Local Similarity 87.5%; Pred. No. 11;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAWDDSL 8
 Db 108 AAWDDSLN 115

RESULT 13
 S25754
 IG lambda chain - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C;Accession: S25754
 R;Combiarto, G.; Kiobeck, H.G.
 Eur. J. Immunol. 21, 1513-1522, 1991
 A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
 A;Reference number: S16439; MUID:91257162; PMID:1904362
 A;Accession: S25754
 A;Status: preliminary; translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-235 <COM>
 A;Cross-references: EMBL:X57819; NID:g33737; PIDN:CAA40956.1; PID:g33738
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;150-218/Domain: immunoglobulin homology <IMM>

Query Match 69.0%; Score 40; DB 2; Length 235;
 Best Local Similarity 87.5%; Pred. No. 11;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAWDDSL 8
 Db 108 AAWDDSLN 115

RESULT 14
 E87394
 conserved hypothetical protein CC1169 [imported] - Caulobacter crescentus
 C;Species: Caulobacter crescentus
 C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
 C;Accession: E87394
 R;Niernman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A;Title: Complete Genome Sequence of Caulobacter crescentus.
 A;Reference number: A87249; MUID:21173698; PMID:11259647
 A;Accession: E87394
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-355 <STO>
 A;Cross-references: UNIPROT:Q9A325; GB:AE005673; NID:g13422491; PIDN:AAK23153.1; GSPDB:C
 C;Genetics:
 A;Gene: CC1169

Query Match 69.0%; Score 40; DB 2; Length 355;
 Best Local Similarity 87.5%; Pred. No. 18;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAWDDSL 8
 Db 138 SAWDDSL 145

RESULT 15

G95983
 probable glycerol kinase (EC 2.7.1.30) [imported] - Sinorhizobium meliloti (strain 1021)
 C;Species: Sinorhizobium meliloti
 C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
 C;Accession: G95983
 R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernanc
 Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
 A;Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing endo
 A;Reference number: A95842; MUID:21396508; PMID:11481431
 A;Accession: G95983
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-497 <KUR>
 A;Cross-references: UNIPROT:O86033; GB:AL591985; PIDN:CAC49535.1; PID:g15141022; GSPDB:G
 A;Experimental source: strain 1021, megaplasmid pSymB
 R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, P.; Barloy-Hubler,
 pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
 hebaullt, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C
 A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A;Reference number: A96039; MUID:21368234; PMID:11474104
 A;Contents: annotation
 C;Genetics:
 A;Gene: glpK; Smb21009
 A;Genome: plasmid
 C;Superfamily: xylulokinase
 C;Keywords: phosphotransferase

Query Match 69.0%; Score 40; DB 2; Length 497;
 Best Local Similarity 70.0%; Pred. No. 26;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAWDDSLSEFL 11
 Db 197 AAWDDSLTEVL 206

Search completed: October 14, 2005, 16:23:41
 Job time : 16.2969 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2005, 15:51:44 ; Search time 73.2188 Seconds
(without alignments)
76.932 Million cell updates/sec

Title: US-10-614-959-15
Perfect score: 58
Sequence: 1 AAWDDSLSEFL 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	75.9	108	Q96SB0	Q96sb0 homo sapien
2	43	74.1	236	Q8NEJ1	Q8nej1 homo sapien
3	43	74.1	628	Q6CLT9	Q6clt9 kluyveromyc
4	41	70.7	112	LV1H_HUMAN	P06887 homo sapien
5	41	70.7	237	Q6DHW4	Q6dhw4 homo sapien
6	40	69.0	109	LV1F_HUMAN	P04208 homo sapien
7	40	69.0	355	Q9A925	Q9a925 caulobacter
8	40	69.0	376	CEA2_RAT	Q91k15 rattus norv
9	40	69.0	381	CEA2_HUMAN	Q9nfp8 homo sapien
10	40	69.0	381	CEA2_MOUSE	Q8r2v5 mus musculu
11	40	69.0	497	GLPK_RHIME	Q86033 rhizobium m
12	40	69.0	502	Q48904	Q48904 microcystis
13	40	69.0	1714	YP93_CABEL	Q09475 caenorhabdi
14	40	69.0	4367	DYHC_NEUCR	P45443 neurospora
15	39	67.2	182	Q87GV3	Q87gv3 vibrio para
16	39	67.2	236	Q8GMV7	Q8gmv7 homo sapien
17	39	67.2	397	KAPI_BOVIN	P24256 bos taurus
18	39	67.2	398	Q723M1	Q723m1 homo sapien
19	39	67.2	578	Q8W0B5	Q8w0b5 oryza sativ
20	39	67.2	751	Q6C021	Q6c021 yeastowia li
21	39	67.2	894	Q74B13	Q74b13 geobacter s
22	39	67.2	969	Q7RYB3	Q7ryb3 neurospora
23	39	67.2	1466	Q98TR8	Q98tr8 bufo bufo (
24	39	67.2	1995	YCX7_CHLRE	P36495 chlamydomon
25	39	67.2	4344	DYHC_EMENI	P45444 emericeella
26	38	65.5	170	Q73YE0	Q73ye0 mycobacteri
27	38	65.5	215	Q67NP3	Q67np3 symbiobacte
28	38	65.5	244	Q31358	Q31358 brachydanio
29	38	65.5	252	Q631V6	Q631v6 bacillus ce
30	38	65.5	252	Q72Y69	Q72y69 bacillus ce
31	38	65.5	252	Q815W5	Q815w5 bacillus ce

RESULT 1
Q96SB0 ID Q96SB0 PRELIMINARY; PRT; 108 AA.
AC Q96SB0;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Anti-streptococcal/anti-myoisin immunoglobulin lambda light chain
DS Variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Anderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myoisin
RT antibody V region genes."; J. Immunol. 161:2020-2031(1998).
RL EMBL; U96394; AAB68783.1; -.
DR PDB; 1KU4; Model; L=1-108.
DR InterPro; IPR007110; IG-like.
DR SMART; SMART; IPR003596; IG_v.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
SQ SEQUENCE 108 AA; 11594 MW; F4B5DC478A043F48 CRC64;
Query Match 75.9%; Score 44; DB 2; Length 108;
Best Local Similarity 72.7%; Pred. No. 3.1;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAWDDSLSEFL 11
Db 90 AAWDDSLSEFL 100
RESULT 2
Q8NEJ1 ID Q8NEJ1 PRELIMINARY; PRT; 236 AA.
AC Q8NEJ1;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;

32 38 65.5 252 2 Q81X10 Q81x10 bacillus an
33 38 65.5 252 2 Q6HBP1 Q6hbp1 bacillus th
34 38 65.5 299 2 Q74E50 Q74e50 geobacter s
35 38 65.5 302 1 DAPA_XANAC Q8pln5 xanthomonas
36 38 65.5 329 1 SRA3_CAEEL Q09205 caenorhabdi
37 38 65.5 348 2 Q9F6D9 Q9f6d9 streptomyc
38 38 65.5 395 2 Q6R8A6 Q6r8a6 sodalis glo
39 38 65.5 443 2 Q76S23 Q76s23 molluscum c
40 38 65.5 496 2 Q83155 Q83155 molluscum c
41 38 65.5 514 2 Q7WZ48 Q7wz48 nonomuraea
42 38 65.5 605 1 PLB1_CANAL Q9b091 mycobacteri
43 38 65.5 842 1 AGGC_SCOLI Q9uwf6 candida alb
44 38 65.5 869 1 RIR3_YEAST P46005 escherichia
45 38 65.5 869 1 RIR3_YEAST P21672 saccharomyc

RA Nicaud J.M., Nikolaï M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potter S., Richard G.F., Straub M.L., Suleau A.,
RA Swenne D., Tekai F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Winker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=NRRL Y-1140;
RC Genoscope;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; CR382126; CAG97807.1; --:calcium ion storage activity; IEA.
DR GO; GO:0005514; F:calcium ion storage activity; IEA.
DR InterPro; IPR001580; Calret/calnex.
DR InterPro; IPR008985; ConA like lec_gl.
DR Pfam; PF00262; Calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calret/calnex; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 1.
SQ SEQUENCE 628 AA; 70981 MW; B0D9A6D1A64644EE CRC64;

Query Match 74.1%; Score 43; DB 2; Length 628;
Best Local Similarity 66.7%; Pred. No. 32;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps

QY 3 WDDSLSEFL 11
|||||:
DB 309 WDDSISEVI 317

RESULT 4
LV1H HUMAN ID LV1H HUMAN STANDARD; PRT; 112 AA.
AC P06887;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda chain V-I region MEM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RX [1]
RP SEQUENCE.
RX MEDLINE=85257662; PubMed=2410269;
RA Mihaesco E., Roy J.P., Congy N., Peran-Rivat L., Mihaesco C.;
RT "The amino acid sequence of a lambda light chain presenting abnormal
RT physicochemical and antigenic features.";
RL Eur. J. Biochem. 150:349-357(1985).
CC -1- MISCELLANEOUS: Residues 33-36 and some of the sequenced peptides
CC were positioned by homology.
CC -1- MISCELLANEOUS: The C region of this chain has the Mcg+ and Kern+
CC markers.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A25479; LIHUMM.
DR HSSP; P01703; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR Direct protein sequencing; Immunoglobulin V region;
KW Monoclonal antibody; Pyrrolidone carboxylic acid.
FT DOMAIN 1 106 Ig-like.
FT MOD RES 1 1 Pyrrolidone carboxylic acid.
FT DISULFID 22 90 By similarity.
FT NON_TER 112 112

SEQUENCE 112 AA; 11789 MW; 748124F079CFFBE4 CRC64;
Query Match 70.7%; Score 41; DB 1; Length 112;
Best Local Similarity 63.6%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAWDDSLSEFL 11
DB 91 AAWDDSLDGVY 101

RESULT 5
Q6DHW4 PRELIMINARY; PRT; 237 AA.
ID Q6DHW4
AC Q6DHW4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Lequellano N.A., McKernan K.J., Agramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwen P.J., Peters G.J., Casavant T.L., Scheetz T.E.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC075843; AAY75843.1; -;
DR InterPro; IPR003599; IG;
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003596; IG v.
DR Pfam; PF07654; cl-bet; 1.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 237 AA; 25108 MW; 6814170F7E784825 CRC64;

Query Match 70.7%; Score 41; DB 2; Length 237;
Best Local Similarity 87.5%; Pred. No. 26;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDDSLS 8

DB 109 AAWDDSMS 116
|||||:|
RESULT 6
LV1F HUMAN STANDARD; PRT; 109 AA.
ID LV1F HUMAN
AC P04208;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda chain V-I region WAH.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83221661; PubMed=6407018;
RA Takahashi Y., Takahashi N., Teraert D., Putnam F.W.;
RT "Complete covalent structure of a human immunoglobulin D: sequence of
the lambda light chain.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:3686-3690 (1983).
DR PIR; A01967; L1HUWA.
DR HSP; P01703; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 97 V segment.
FT DISULFID 22 89 J segment.
FT NON TER 109 109 By similarity.
SQ SEQUENCE 109 AA; 11725 MW; B17785F6A8DF9BAC CRC64;

Query Match 69.0%; Score 40; DB 1; Length 109;
Best Local Similarity 80.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAWDDSLSEFL 10
DB 90 AAWDDSLWVF 99
|||||:|

RESULT 7
Q9A925 PRELIMINARY; PRT; 355 AA.
ID Q9A925
AC Q9A925;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein CC1169.
GN OrderedLocustNames=CC1169;
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Kouri H.M., Shetty J.,
RA Berry K.J., Utterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,
RA Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,

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RA  Fraser C.M.;
RT  "Complete genome sequence of Caulobacter crescentus.";
RL  Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR  EMBL; AR005795; AAK23153.1; -.
DR  PIR; E87394; E87394.
DR  TIGR; CCL169; -.
DR  InterPro; IPR011251; Luciferase_like.
DR  Pfam; PF00296; Bac_luciferase; 1.
KW  Complete proteome; Hypothetical protein.
SQ  SEQUENCE 355 AA; 38552 MW; 3C4AEF42825E567 CRC64;

Query Match          69.0%; Score 40; DB 2; Length 355;
Best Local Similarity 87.5%; Pred. No. 63;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  1 AAWDDSL 8
DB  138 SAWDDSL 145

RESULT 8
CEA2 RAT
ID  CEA2_RAT STANDARD; PRT; 376 AA.
AC  OSJL5;
DT  25-OCT-2004 (Rel. 45, Created)
DT  25-OCT-2004 (Rel. 45, Last sequence update)
DT  25-OCT-2004 (Rel. 45, Last annotation update)
DE  Centaurin alpha 2.
GN  Names=Cent2;
OS  Rattus norvegicus (Rat).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX  NCBI_TaxID=10116;
RN  [1]
RP  SEQUENCE FROM N.A., INTERACTION WITH PTDINS(4,5)P2, PTDINS(3,4,5)P3
RP  AND INS(1,3,4,5)P4, TISSUE SPECIFICITY, AND MUTAGENESIS OF ARG-151 AND
RP  ARG-275.
RC  TISSUE=Adipocyte;
RX  MEDLINE=22012451; PubMed=12018390;
RA  Whitely P., Gibbard A.M., Koumanov F., Oldfield S., Kilgour E.E.,
RA  Prestwich G.D., Holman G.D.;
RT  "Identification of centaurin-alpha2: a phosphatidylinositol-binding
RL  protein present in fat, heart and skeletal muscle.";
RL  Eur. J. Cell Biol. 81:222-230(2002).
CC  -1- FUNCTION: GTPase-activating protein for the ADP ribosylation
CC  factor family (Potential).
CC  -1- SUBUNIT: Binds phosphatidylinositol 4,5-bisphosphate,
CC  phosphatidylinositol 3,4,5-trisphosphate (PtdInsP3) and inositol
CC  1,3,4,5-tetrakisphosphate (InsP4). Binding of phosphatidylinositol
CC  3,5-bisphosphate and phosphatidylinositol 3,4-bisphosphate occurs
CC  at a much lower affinity. Possesses a stoichiometry of two binding
CC  sites for InsP4 with identical affinity (By similarity).
CC  -1- SUBCELLULAR LOCATION: Cytoplasmic. Constitutively associated with
CC  the plasma membrane. Excluded from the nucleus (By similarity).
CC  -1- TISSUE SPECIFICITY: Expressed in many tissues, with highest levels
CC  in fat, heart and skeletal muscle. Also detected in kidney, liver
CC  and lung.
CC  -1- SIMILARITY: Contains 1 Arf-GAP domain.
CC  -1- SIMILARITY: Contains 2 PH domains.
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  EMBL; AJ238993; CAB88403.1; -.
DR  RGD; 708487; LOC56826.
DR  InterPro; IPR001164; hRIP-like.
DR  InterPro; IPR001849; PH.
DR  InterPro; IPR011036; PH_related.

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DR  Pfam; PF01412; ArfGAP; 1.
DR  Pfam; PF00169; PH; 2.
DR  PRINTS; PR00405; REVINTRACTING.
DR  SMART; SM00105; ArfGAP; 1.
DR  SMART; SM00233; PH; 2.
DR  PROSITE; PS01115; ARFGAP; 1.
DR  PROSITE; PS00003; PH_DOMAIN; 2.
KW  GTPase activation; Metal-binding; Repeat; Zinc; Zinc-finger.
FT  DOMAIN 9 130 Arf-GAP.
FT  ZN_FING 25 48 C4-type.
FT  DOMAIN 131 232 PH 1.
FT  DOMAIN 254 360 PH 2.
FT  MUTAGEN 151 151 R->C: Almost complete loss of InsP4
FT  MUTAGEN 275 275 R->C: No loss of InsP4 binding. Almost
FT  MUTAGEN 275 275 complete loss of InsP4 binding; when
FT  associated with C-151.
SQ  SEQUENCE 376 AA; 43524 MW; E357392F38F07166 CRC64;

Query Match          69.0%; Score 40; DB 1; Length 376;
Best Local Similarity 66.7%; Pred. No. 67;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY  3 WDDSLSEFL 11
DB  69 WDDSMVEFM 77

RESULT 9
CEA2 HUMAN
ID  CEA2_HUMAN STANDARD; PRT; 381 AA.
AC  Q2NP8; OBN4Q6; Q96SD5;
DT  28-FEB-2003 (Rel. 41, Created)
DT  28-FEB-2003 (Rel. 41, Last sequence update)
DT  25-OCT-2004 (Rel. 45, Last annotation update)
DE  Centaurin alpha 2.
GN  Name=CENTA2;
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A. (ISOFORM 1).
RX  MEDLINE=22012451; PubMed=12018390;
RA  Whitely P., Gibbard A.M., Koumanov F., Oldfield S., Kilgour E.E.,
RA  Prestwich G.D., Holman G.D.;
RT  "Identification of centaurin-alpha2: a phosphatidylinositol-binding
RL  protein present in fat, heart and skeletal muscle.";
RL  Eur. J. Cell Biol. 81:222-230(2002).
CC  -1- SEQUENCE FROM N.A. (ISOFORM 1).
CC  MEDLINE=20304757; PubMed=10843809; DOI=10.1006/geno.2000.6179;
CC  Jenne D.E., Tinschert S., Stegmann E., Reimann H., Nurnberg P.,
CC  Horn D., Naumann I., Buske A., Thiel G.;
CC  "A common set of at least 11 functional genes is lost in the majority
CC  of NF1 patients with gross deletions.";
CC  Genomics 66:93-97(2000).
CC  [3]
CC  SEQUENCE FROM N.A. (ISOFORM 1).
CC  SEQUENCE FROM N.A. (ISOFORM 1).
CC  Bertsch U., Illies C., Mayr G.W.;
CC  Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC  [4]
CC  SEQUENCE FROM N.A. (ISOFORM 2).
CC  TISSUE=Leukocyte;
CC  MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
CC  Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
CC  Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
CC  Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
CC  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
CC  Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
CC  Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
CC  Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
CC  Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

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Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Marra M.A.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[5]
RP INTERACTION WITH PTDINS(3,4,5)P3 AND INS(1,3,4,5)P4, TISSUE
RP SPECIFICITY, AND SUBCELLULAR LOCATION.
RX PubMed:14690521;
RA Hanck T., Stricker R., Sedehezade F., Reiser G.;
RT "Identification of gene structure and subcellular localization of
RT human centaurin alpha 2, and p21IP4, a family of two highly
RT homologous, Ins 1,3,4,5-P4-(Ptdins 3,4,5-P3-binding, adapter
RT proteins.";
RL J. Neurochem. 88:326-336(2004).
CC -!- FUNCTION: GTPase-activating protein for the ADP ribosylation
CC factor family (Potential).
CC -!- SUBUNIT: Binds phosphatidylinositol 3,4,5-trisphosphate (PtdInsP3)
CC and inositol 1,3,4,5-tetrakisphosphate (InsP4). Possesses a
CC stoichiometry of two binding sites for InsP4 with identical
CC affinity.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic. Constitutively associated with
CC the plasma membrane. Excluded from the nucleus.
CC -!- ALTERNATIVE PRODUCTS;
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9NPF8-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9NPF8-2; Sequence=VSP_011180;
CC Note=May be due to a competing acceptor splice site. No
CC experimental confirmation available;
CC -!- TISSUE SPECIFICITY: Highly expressed in placenta, spleen, kidney,
CC skeletal muscle and adrenal gland. Weakly expressed in thyroid,
CC liver, heart, lung, small intestine, peripheral blood leukocytes.
CC Not detected in spinal cord, brain, stomach, trachea, colon, lymph
CC node and bone marrow.
CC -!- SIMILARITY: Contains 1 Arf-GAP domain.
CC -!- SIMILARITY: Contains 2 PH domains.
CC
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CC
CC EMBL; AJ238994; CAB88383.1; -
CC EMBL; AJ272195; CAB77266.1; -
CC EMBL; AJ242782; CAC40651.1; -
CC EMBL; BC033758; AAH33758.1; -
CC Genew; HGNC:16487; CENTA2.
CC H-InvDB; HIX001369; -
CC MIM; 608635; -
CC InterPro; IPR001164; hRIP_like.
CC InterPro; IPR001849; PH.
CC InterPro; IPR011036; PH related.
CC Pfam; PF01412; ArfGAP; 1.
CC Pfam; PF00169; PH; 2.
CC PRINTS; PR00405; REVINTRACTNG.
CC SMART; SM00105; ArfGap; 1.
CC SMART; SM00233; PH; 2.
CC PROSITE; PS50115; ARFGAP; 1.
CC PROSITE; PS50003; PH_DOMAIN; 2.
CC Alternative splicing; GTPase activation; Metal-binding; Repeat; Zinc;
CC Zinc-finger.

FT DOMAIN 9 131 Arf-GAP.
FT ZN FING 25 48 C4-type.
FT DOMAIN 132 233 PH 1.
FT DOMAIN 255 361 PH 2.
FT VARSP LIC Missing (in isoform 2).
FT /FTID=VSP_011180.
FT CONFLICT 12 12 L -> P (in Ref. 3).
SQ SEQUENCE 381 AA; 44348 MW; 4FAE208072A92C01 CRC64;
Query Match 69.0%; Score 40; DB 1; Length 381;
Best Local Similarity 66.7%; Pred. No. 68;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 3 WDSLSSEFL 11
Db 69 WDSLSSEFL 77
RESULT 10
CEA2 MOUSE
ID CEA2 MOUSE STANDARD; PRT; 381 AA.
AC Q8R2V5;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DE 25-OCT-2004 (Rel. 45, Last annotation update)
DE Centaurin alpha 2.
GN Name=Cent2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Breast tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buotow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Marra M.A.,
RA Schnersch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: GTPase-activating protein for the ADP ribosylation
CC factor family (Potential).
CC -!- SUBUNIT: Binds phosphatidylinositol 3,4,5-trisphosphate (PtdInsP3)
CC and inositol 1,3,4,5-tetrakisphosphate (InsP4). Possesses a
CC stoichiometry of two binding sites for InsP4 with identical
CC affinity (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic. Constitutively associated with
CC the plasma membrane. Excluded from the nucleus (By similarity).
CC -!- SIMILARITY: Contains 1 Arf-GAP domain.
CC -!- SIMILARITY: Contains 2 PH domains.
CC
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DR EMBL; AL591985; CAC49535.1; -;
DR EMBL; AF080548; AAD12735.1; -;
DR PIR; G95983; G95983.
DR HSSP; P08859; 1GLC.
DR HAMAP; MF_00186; -; 1.
DR InterPro; IPR000577; FGGY_kin.
DR InterPro; IPR005999; Glycerol_kin.
DR Pfam; PF02782; FGGY_C; 1.
DR Pfam; PF00370; FGGY_N; 1.
DR TIGRfam; TIGR01311; glycerol_kin; 1.
DR PROSITE; PS00933; FGGY_KINASES_1; FALSE_NEG.
DR PROSITE; PS00445; FGGY_KINASES_2; 1.
DR KW ATP-binding; Complete proteome; Glycerol metabolism; Kinase; Plasmid;
KW Transferase.
FT NP BIND 153 165 ATP (Probable).
SQ SEQUENCE 497 AA; 54419 MW; 42D3428335ACC2B7 CRC64;

Query Match 69.0%; Score 40; DB 1; Length 497;
Best Local Similarity 70.0%; Pred. No. 90;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 AWDSLSEFL 11
Db 197 AWDELTEVL 206
|||||:|:
|:|:|:|:|

RESULT 12
Q48904 PRELIMINARY; PRT; 502 AA.
AC Q48904;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ORF2.
OS Microcystis aeruginosa.
OC Bacteria; Cyanobacteria; Chroococcales; Microcystis.
OX NCBI_TaxID=1126;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HUB 5-2-4;
RA Juerchott K., Boerner T.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z28337; CAA82191.1; -;
DR PIR; S49113; S49113.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR007936; VirE.
DR Pfam; PF05272; VirE; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN 1.
SQ SEQUENCE 502 AA; 58859 MW; 98E61D5C214520E6 CRC64;

Query Match 69.0%; Score 40; DB 2; Length 502;
Best Local Similarity 60.0%; Pred. No. 91;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 AWDSLSEFL 11
Db 434 SWEDELAFL 443
||:|:|:|:
:|:|:|:|

RESULT 13
YP93_CABEL
ID YP93_CABEL STANDARD; PRT; 1714 AA.
AC Q09475;
DT 01-NOV-1995 (Rel. 32, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Putative helicase C28H8.3 (EC 3.6.1.-).

CC EMBL; BC027165; AAH27165.1; -;
DR MGD; MGI:2663075; Centa2.
DR InterPro; IPR001164; hRIP_like.
DR InterPro; IPR001849; PH.
DR InterPro; IPR011036; PH_related.
DR Pfam; PF01412; ArfGap; 1.
DR Pfam; PF00169; PH; 2.
DR PRINTS; PR00405; REVINTRACTNG.
DR SMART; SM00105; ArfGap; 1.
DR SMART; SM00233; PH; 2.
DR PROSITE; PS0115; ARFGAP; 1.
DR PROSITE; PS50003; PH_DOMAIN; 2.
KW GTPase activation; Metal-binding; Repeat; Zinc; Zinc-finger.
FT DOMAIN 9 132 Arf-GAP.
FT ZN FING 25 48 C4-type.
FT DOMAIN 132 233 PH 1.
FT DOMAIN 255 361 PH 2.
SQ SEQUENCE 381 AA; 43989 MW; 2E504CEF0ACD84D5 CRC64;

Query Match 69.0%; Score 40; DB 1; Length 381;
Best Local Similarity 66.7%; Pred. No. 68;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 WDSLSEFL 11
Db 69 WDDSMVEFM 77
|||||:|:
|:|:|:|:|

RESULT 11
GLPK_RHIME
ID GLPK_RHIME STANDARD; PRT; 497 AA.
AC O86033;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Glycerol kinase (EC 2.7.1.30) (ATP:glycerol 3-phosphotransferase)
DE (Glycerokinase) (GK)
GN Name=gpk; OrderedLocNames=RB1135; ORFNames=SMB21009;
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Plasmid pSymB (megaplasmid 2).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RE MEDLINE=21396508; PubMed=11481431; DOI=10.1073/pnas.161294698;
RX Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
RA Vorholter F.J., Hernandez-Lucas I., Becker A., Gouzy J.,
RA Golding B., Fuchler A.;
RA "The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-
fixing endosymbiont Sinorhizobium meliloti.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
RN [2]

SEQUENCE OF 1-59 FROM N.A.
RP STRAIN=S047 / 1021;
RX MEDLINE=99121023; PubMed=9922248;
RA Aneja P., Charles T.C.;
RA "Poly-3-hydroxybutyrate degradation in Rhizobium (Sinorhizobium)
RT meliloti: isolation and characterization of a gene encoding 3-
RT hydroxybutyrate dehydrogenase.";
RL J. Bacteriol. 181:849-857(1999).
CC -1- FUNCTION: Key enzyme in the regulation of glycerol uptake and
CC metabolism.
CC -1- CATALYTIC ACTIVITY: ATP + glycerol = ADP + sn-glycerol 3-
CC phosphate.
CC -1- PATHWAY: Glycerol utilization; rate-limiting step.
CC -1- SIMILARITY: Belongs to the fucokinase / gluconokinase /
CC glycerokinase / xylulokinase family.
CC -----

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GN ORFNames=C28H8.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
ON NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology";
RL Science 282:2012-2018(1998).
RN [2]
RP REVISIONS.
RA Waterston R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -1- SIMILARITY: Belongs to the helicase family. SKI2 subfamily.
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CC -----
DR EMBL; U20861; AAA62291.2; C28H8.3.
DR WormBase; WBGene00016194; C28H8.3.
DR WormPepe; C28H8.3; CE29195.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELICC; 1.
DR TIGRFAMs; TIGR01870; cas TM1810; 2.
DR ATP-binding; Helicase; Hydrolase; Hypothetical protein;
KW Nuclear protein.
FT NP_BIND 607 614 ATP (Potential).
FT NP_BIND 806 813 ATP (Potential).
FT SITE 913 916 DEVH box.
SQ SEQUENCE 1714 AA; 194095 MW; 0936764D27C7EFAD CRC64;

Query Match 69.0%; Score 40; DB 1; Length 1714;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 AAWDDSLSE 9
Db 5 AAWDDSDSE 13
|||||

RESULT 14
DYHC NEUCR STANDARD; PRT; 4367 AA.
ID P45443; O7RVH1;
AC 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Dynein heavy chain, cytosolic (DYHC).
GN Name=ro-1; ORFNames=NCU06976.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
ON NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=74-OR23-1A / FGSC 987;
RX MEDLINE=95014704; PubMed=7929559; DOI=10.1083/jcb.127.1.1139;
RA Plamann M., Minke P.F., Tinsley J.H., Bruno K.S.;
RT "Cytoplasmic dynein and actin-related protein Arp1 are required for
normal nuclear distribution in filamentous fungi";
J. Cell Biol. 127:139-149(1994).
SEQUENCE FROM N.A.
STRAIN=74-OR23-1A / FGSC 987;
PubMed=12712197; DOI=10.1038/nature01554;
Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
Elkins T., Engle R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
Qui D., Ianakiev P., Bell-Pedersen D., Nelson M.A.,
Werner-Washburne M., Selitrennikoff C.P., Kinsey J.A., Braun E.L.,
Zelter A., Schulte U., Kothe G.O., Jedd G., Mewes H.-W., Staben C.,
Marcotte E., Greenberg D., Roy A., Foley K., Naylor J.,
Stange-Thomann N., Barrett R., Gnarr S., Kamal M., Kanvaseelis M.,
Mauceli E., Bielke C., Rudd S., Frishman D., Krystofova S.,
Rasmussen C., Metznerberg R.I., Perkins D.D., Kroken S., Cogoni C.,
Macino G., Catchside D., Li W., Pratt R.J., Osmari S.A.,
Desouza C.P., Glass L., Orbach M.J., Berglund J.A., Voelker R.,
Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
Paulsen I., Sachs M.S., Lander E.S., Nudbaum C., Birren B.;
RT "The genome sequence of the filamentous fungus Neurospora crassa";
Nature 422:859-868(2003).
CC -1- FUNCTION: Cytoplasmic dynein acts as a motor for the intracellular
CC retrograde motility of vesicles and organelles along microtubules.
CC Dynein has ATPase activity; the force-producing power stroke is
CC thought to occur on release of ADP. Required to maintain uniform
CC nuclear distribution in hyphae.
CC -1- SUBUNIT: Consists of at least two heavy chains and a number of
CC intermediate and light chains.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- DOMAIN: Dynein heavy chains probably consist of an N-terminal stem
CC (which binds cargo and interacts with other dynein components),
CC and the head or motor domain. The motor contains six tandemly-
CC linked AAA domains in the head, which form a ring. A stalk-like
CC structure (formed by two of the coiled coil domains) protrudes
CC from AAA 4 and AAA 5 and terminates in a microtubule-binding
CC site. A seventh domain may also contribute to this ring; it is not
CC clear whether the N-terminus or the C-terminus forms this extra
CC domain. There are four well-conserved and two non-conserved ATPase
CC sites, one per AAA domain. Probably only one of these (within AAA
CC 1) actually hydrolyzes ATP, the others may serve a regulatory
CC function.
CC -1- SIMILARITY: Belongs to the dynein heavy chain family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; L31504; AAA64908.1; -;
DR EMBL; AABX0100204; ERA33380.1; -;
DR PIR; B54802; B54802.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR004273; Dynein_heavy.
DR Pfam; PF03028; Dynein_heavy; 1.
DR SMART; SM00382; AAA; 3.
KW ATP-binding; Coiled coil; Dynein; Microtubule; Motor protein; Repeat.
FT DOMAIN 1 1904 Stem (By similarity).
FT DOMAIN 1905 2130 AAA 1 (By similarity).
FT DOMAIN 2202 2460 AAA 2 (By similarity).
FT DOMAIN 2566 2815 AAA 3 (By similarity).
FT DOMAIN 2909 3179 AAA 4 (By similarity).
FT DOMAIN 3193 3481 Stalk (By similarity).
FT DOMAIN 3565 3794 AAA 5 (By similarity).
FT DOMAIN 4003 4215 AAA 6 (By similarity).
FT DOMAIN 676 693 Coiled coil (Potential).
FT DOMAIN 1176 1215 Coiled coil (Potential).
FT DOMAIN 1327 1351 Coiled coil (Potential).
FT DOMAIN 1557 1574 Coiled coil (Potential).

FT DOMAIN 1637 1668 Coiled coil (Potential).
FT DOMAIN 2195 2218 Coiled coil (Potential).
FT DOMAIN 3193 3296 Coiled coil (Potential).
FT DOMAIN 3423 3481 Coiled coil (Potential).
FT DOMAIN 3778 3809 Coiled coil (Potential).
FT NP_BIND 1943 1950 ATP (Potential).
FT NP_BIND 2240 2247 ATP (Potential).
FT NP_BIND 2605 2612 ATP (Potential).
FT NP_BIND 2947 2954 ATP (Potential).
SQ SEQUENCE 4367 AA; 495568 MW; 1E10F3E2D170D6DF CRC64;

Query Match 69.0%; Score 40; DB 1; Length 4367;
Best Local Similarity 66.7%; Pred. No. 9.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 AWDDSLSEF 10
|||:|:|
Db 455 AWDESIKEF 463

RESULT 15

Q87GV3 PRELIMINARY; PRT; 182 AA.
AC Q87GV3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein VPA1212.
GN OrderedLocusNames=VPA1212;
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RIMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";
RL Lancet 361:743-749(2003).
DR EMBL; AF005088; BAC62555.1; -;
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 182 AA; 21333 MW; 2559BEC89FD78332 CRC64;

Query Match 67.2%; Score 39; DB 2; Length 182;
Best Local Similarity 50.0%; Pred. No. 47;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AAWDSLSEF 10
:|:|:|:|:
Db 27 SSDDNLQTF 36

Search completed: October 14, 2005, 16:19:59
Job time : 75.2188 secs